

FIGURE 1

CCAGGTCCAAC TGACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCACCCGGAGG
AGCAGCTCTGCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCC
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACATTTATAGGACCGCCTAC
CGCCGAGCCCTGGGCTGGCCCTGCCAGGCCTCGCTACGCGTGC TGCCCCGGCTGGAAGAG
GACCAGCGGCTTCTTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCA GTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGACCCCGGCAGCC
TCCTGGTGC ACTCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTC
CTGGAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGA CTGCCAGCGCCCCAGG
CTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTG
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTTTTCTCCTC
CCCTTCTCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGTGGGATTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCCTGTGAGCCTGGGACCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCCTCAGTGGGGCTGTGCTGACCCCGAGCACAATAAAATGAAA
CGTGA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCATGCCCCA ACTGTGTTATTGCGACTTATAATGGT
TACAAAT

FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVSGSRHRARLPARPLGCVLSRAHGDPV
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTL CVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCCGTGCGCCCTCGCCTCCCCGACAGTCCCCTCGCGGCAGCAGATGTTGTGCGG
 GTCAGCCCCACGGCGGGGACTATGTTGAAATCCCAGCGCTCACGCACTACTGGCCCCCTGATC
 CGGTTCTTGGTGGCCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA
 CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT
 ACTCCCTCATGAAGTTCCTCACGGGTCCCATGAGTGACTTCAAAAAATGTGGGCCTGGTGTTT
 GTGAAACAGCAAGAGAGACAGGACCAAAGCCGCTCCTGTGTATGTTGGTGGGACGGGCGCATCGC
 TGCCGCTCTTTACACACTGATAGCTTTATAGTGATTAGGATACTACATTATCAATAAACTGC
 ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCCTTCTGTACTCTCGCCGCTCTT
 CCTTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT
 CCTGGTGGGATGTGCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC
 TTCACAGTCACCTGGAATGCGGGAGCCCCGCTCATCCCCGATCCTCTCCTGTACATGGGC
 GCATCTGTGCGCTGCACCAACCCTGTGCTGGGCTACTACAAGAACATTCACGACATCATCCC
 TGACAGAAGTGGCCCCGGAGCTGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
 GGCCTTTGGCTCTAATTTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTGTT
 TCCCGGGACCTTGGTGGCATTCTGCAGCCACAGAGGCGAGTGGCGCATTTTGCACGCCACATA
 CCCGTGTGGGTACATGCCATAACGCTGGTTGACGGAAATCCGCTCTGTGTATCCTGCTTTTCG
 ACAAGAATAACCCGACCAACAACCTGGTGAGCACGAGCAACAGTCACGGCAGCCCATATC
 AAGAAGTTCACTTCTGCTGTGATGGCTCTGTCACTCACGCTCTGTTTCTGTGATGTTTTGGAC
 ACCCAACGTGTCTGAGAAAAATCTGTATAGACATCATCGGAGTGGACTTTGCCTTTGCGAAAC
 TCTGTCTGTTGCTTCTTTGGGATCTTCTCCTTCTTCCGACTCCAGTCACAGTGGGCGCATC
 CTCACCGGTGGCTGATGACACTGAAGAAACCTTCTGCTTGCCTCCAGCTCTGTGCTGCG
 GATCATCGTCCCTCATCGCCAGCCTCGTGGTCTACCTACCTGCGGGGTGCAGGTCGACCC
 TGGCGTGGGCTCCCTCTGCGGGGCTTTGTGGGAGAATCCACCATAGTTCGCCATCGCTGCG
 TGCTATGTCTACCGGAAGCAGAAAAAGAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA
 CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGG
 AGAATGAATAAGGACCGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC
 GGCATCATCTCTCCCTCTCCCATCGTATTTTGTTCCTTTTCTTTTGTGTTTGTGTTTGGTAAT
 GAAAGAGGCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACT
 GACGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAACGAAACAACCTGAC
 TTTATACCCCTGCTCAGAAAAACCAAAGACACAGCTGCCCTCAGCGTTGACGTTGTGTCTC
 TCTCCCCGGAACAATCTCCTCTGGAAACCAAGGACTGCAGCTGGCCATCGCGCTCGGT
 CACCTGACAGCAGGCGACACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG
 TTAATACTCGGCTTCCCTTGATTGTCTCCAGTCACATGGCCGTACAAGAGATGGAGGCC
 CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGACG
 GAGGCGGGTGGCACGCTGCAGCCCCGAGTCCCCGTTACACTGAGGAACGGAGACCTGTGAC
 CACAGCGGCTGACAGATGGACAGAATCTCCCGTAAAGAGTTTGGTTTGAATGCCCCGGG
 GGCAGCAACTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCTAGATCTGAGCAA
 GCTGTGAGTTCTACCCCCACCGTGTATATACATGAGCTAACTTTTAAATTTGTCAACAAA
 GCGCATCTCAGATTCTCAGACCTGCGCATGACTTTTCTGAGGCTTGCTTTTCCCTCGC
 CTCTCTGAAGGTCGATTTAGAGCGAGTCACATGGAGCATCTTAACCTTTGCAATTTAGTTTT
 TACAGTGAACGTAAGCTTTAGTCTCATCGACATTCTAATGCCAGTGGCTCTAGGGTAAC
 TTTTGAAGTAGATATATTACCTGGTCTGCTATCCTTAGTCATACTCTGCGGTACAGGTAA
 TTGAGAAATGTAACGCTTCCCTCCCACACCATACGATAAAGCAAGACATTTATAACG
 ATACAGAGTCACTATGTGGTCTCCTCGTAAATAACGCAATTCGAATCCATGCACTGACGTA
 TATTTTTCTAAGTTTTTGAAAGCAGGTTTTTCTTTAAAAAAATATAGACACGGTTCAT
 AAATTTGATTAGTCAGAAATCTAGACTGAAAGAACCTAAACAAAAAATTTTAAAGATA
 TAAATATATGCTGATATGTTATGTAATTTATTTTAGGCTATAATACATTTCTATTTTCG
 ATTTTCAATAAAATGTCTCTAATAAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSEDFKNVGLVFNNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYIINKLHHVDESV
GSKTRRAFLYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCTTLCGLYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNVTAAHIKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelCVVPLR
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGvHGATLGvGSLl
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPTEEVTDIVEMREENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
 GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
 TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
 CCTGTGGGTCACATGCCATACGGCTGGTTGACGGAATCCGTGCTGTGTATCCTGCTTTCG
 ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCACATC
 AAGAAGTTCACCTTCGTCTGCAATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTGGAC
 ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGAGTGGACTTTGCCTTGCAGAAC
 TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCAGTTCAGTCACAGTGAGGGCGCAT
 CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

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FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTGAGAAAATTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTCAGAAATTTGNGNTGTTCCCTTTCGGATTTTCT
CCTTTTTCCAGTTCCAGTCACAGNGAGGGCGCATCTACCGGGNGGNTGATGACANTGAAG
AAAACCTTTGTCTTGCCCCAGCTNNTTGGTGC GGATCATGTCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGC GACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

1000
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200
100
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FIGURE 7

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

FIGURE 8

GCCCCGCGCCCGCGCCGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCGCTGCCTGGGA
GCCTGCTCCTTGCTCAGCTGCGCGTCTGCTCTGCGGCTTGCCCCCTGCACTCCTGTGCAG
CTGTGTCGCCCGCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCAGTTCTTCTCTTCC
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGCGTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGCGGGATCCCCACCGTCTGCAAGGGCCACATCGACTGTGG
CTCCTGCTTGGTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCTTCTTCTTCT
TCTTTTACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCGGGTGCCTACAG
AATGGGTTTTGGTTCTTTAAGTTCTTGATCCTGGTGGGCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTACCAACATCTGGTTCTACTTCGGCGTCTGGGCTCCTTCTCTTCA
TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACAGCGGTGGTGGGC
AAGGCCGAGGAGTGCATTCCCGTGCCTGGTACGCAAGGCCCTTCTTCTTCACTCTCTCTT
CTACTGCTGTGATCGCGGCGTGGCGCTGATGTTTATGTACTACACTGAGCCAGCGGCT
GCCACGAGGGCAAGGTCTTATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCTGCCCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAAGGCTCGGTGCT
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCATTTTGCAACCCAGCTGGGCAACGAGACAGTTTGGGAGGCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCGAGCATTTGGGGCTCATCATCTTCTCTGTGACCCCTCTT
CATCAGTCTGCGTCTCTAGACCACCGGAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGAGTGGCAGCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACTACAGCTACTCTTCTTCCACTTCTGCTGGTGTCT
GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGAAGA
TGATCAGCACGTGGACCGCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAAGGCTGCTCCTC
TACCTGTGGACCTGGTAGCCCCACTCTCTGCGCAACCGCACTTCACTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT
GCCCCCTCCCCACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG
CCCCGTGAGCCGGGCTTCTAGTCTGATGCTTTCAGGGTCCGAGGAGCATCAGGCTCTTGCA
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCTCTTCTTCCCCCTCTCCTGT
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGG
CTGCTGGAGAGAGCGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT
CCTGGTCACTGCCCCAGGGGACCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTTCTAATAACAAGCCAGTGCCTGTAAAAAAA

FIGURE 9

MGACLGACSLSCASCCLGSA PCILCSCCPASRNSTVSR LIFTFFLFLGVLVSIIMLSPGVE
SQLYKLPWVCEE GAGIPTVLQGHIDCGSL LGYRAVYRMC FATAA FFFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLIILVGLTVGAFYIPDGSFTNIWFFYFGVVG SFLFILIQLVLLIDFAHSW
NQRWL GKAE ECD SRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKV FISLNLTF C
VCV SIAAVLPKVQDAQPN SGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIVGLIIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA
ACEGRAFDNEQDGV TYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 10

GAGCGAGGCCGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTG
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA
AGTCTTGAGCGCTCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG
TGA CTGCCGATTCCGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG
TGTATGGGGGAATACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT
CATTCTGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATTGCAGGA
GCTGTACGGGAAGTCTTTTATAGGATAAACGTAGGCCCTGCGTGGCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACTCTGTAGGAGGCCCTGCTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTTTCAGGAAAAGAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACCTGGAA
GAGTGAAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC
CTTCAGTAATAGATAAACAAGACAAGGACTGAAAGTGCTCTGAACCTGAAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTTTCTTTTCTTTTCTT
TTTAACTAAGAATGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT
TATGTTTGTATTAACTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA
GCAGTAAATAAACATTTTCGCAAAGATTAAAGTTGAATTTTACAGTTT

FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAETVYHNRFDVQSAH
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALS HFVIAGAVTGS LFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGR LQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTTCATG
GCTGGCGCCGAACC

FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

FIGURE 14

GAGCCGCCGCCGCCGCCGCCGCCGCACTGCAGCCCCAGGCCCGGCCCGCCACCCACGTCT
GCGTTGCTGCCCCGCCCTGGGCCAGGCCCAAAGGCAAGGACAAAGCAGCTGTGAGGAACT
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGCCAACCACAGGTTCCAAGATGGTTTGGGGG
GCTTCGCGTGTTCGAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG
CTGCTAATTGGAATTGCTGCGTGGGGCATTTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
CGGCGTGGTCATTGCAGTGGGCATCTTCTGTTCCTGATTGCTTTAGTGGGTCTGATTGGAG
CTGTAAAACATCATCAGGTGTTGCTATTTTTTTATATGATTATCTGTTACTTGTATTTATT
GTTCAGTTTTCTGTATCTTGCCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAACTGCT
GTGGGTTCCGAAGTGTTAACCCAAATGACACCTGCTGGCTAGCTGTGTTAAAGTGACCAC
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG
TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA
GGAACCAGAAAGACCCCCGCCGGAATCCTAGTGCAATTCCTTTGATGAGAAAACAAGGAAGAT
TTCCTTTCGTATTATGATCTTGTTCACCTTCTGTAAATTTCTGTAAAGCTCCATTGCCAGT
TTAAGGAAGGAAACATATCTGGAAGTACCTTATTGATAGTGGAATTATATATTTTTACT
CTATGTTTCTCTACATGTTTTTTCTTCCGTTGCTGAAAAATATTTGAACTTGTGGTCTC
TCTTAGCATTTTTACCTGCAGAAAACTTTGTATGTTACCACTGTGTTGGTTATATGGTGAA
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC
TGAAAAAAGAGTGGAATTTATTAATAATCAGAAAGTATGAGATCCTGTTATGTTAAGGAAA
TCCAAATTCCCAATTTTTTTTTGGTCTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT
GTCTTAGGAAATGTGGTTTAAATTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGTTTT
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA
AAGACTGCATTTTTAAACAAGTTAGTATTAAATGCGTTGGCCACGTAGCAAAAAGATATTTG
ATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAACAGCAACT
GTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATTGTGTG
GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAAACCTTTCTTTGTGTATGCATGTTTGA
ATTAAAAAGAAAGTAATGGAAG

FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIAGVIFLFLIALV
GLIGAVKHHQVLLFFYMIILLVFIQFSVSCACALANQEQQGQLLEVGVNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFRVGGIGLFFSFTEILGVWL
TYRYRNQKDPRANPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCGTAAANT
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTTGTTGGTGGCATTGGCCTGTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

FIGURE 17

AATCCCAAATTCCCCAATTTTGGNCTTTTAGGGAAAGATGTGTGTGGTAAAAAGTGT
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTTAATTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTGTAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGC

FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCCTTGTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCAGCTGAGGAGAGCAGCTGCCACCGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCTTACACTTTCAGTGAACCCCTCCACCTGATTGTGTCTATGACTGGCTG
ATCCTCCAAGGTCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCTTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC
TGCAGTGGCATCTTCCAGAGCCCTGGTCTCGGATCCAGAAACAGCATCTGTTGTGGCTAT
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCCTGAGTTGTACAGACAAAGTTGCCCTGCAGAGGTGAGCTGCCCGC
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCTACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAATGCTCCTGA
GGAGGCCCCCTGGGCTCTGCTCCGCGGCCAACCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGAGTGCCAGATCCTCATCTGTATCACCAGATGGGCTTCTTCTCAACACATG
CAGGATGTGAGAGTCTCTCCTCGGTCACTGCTCATGGAGTTGAGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAAGTAAACAGTTTATCCATGATCTCACT
TAACCACCCCAATAAATCTGATTCTTATTTTCTCTTCTGTCTCTGCACATATGCATAAGTA
CTTTTACAAGTTGTCCAGTGTTTTGTAGAAATATGTAGTTAGGTGAGTGTAATAAATTT
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGCAATTTTGCCCCCAGAGGACA
TTGGGCAATGTTGGAGACATTTGGTCATTATACTTGGGGGGTGGGGGATGGTGGGATGT
GTGCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGTAAACATCCTATAATGCACAG
GGCAGTACCCCAACAAGAAAAATAATCTGGCCCCAAATGTGAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAAACCTAGGTGTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTTCCAGCCTCATTCAGCTATCTTACTGACATACCAGTCTTTAGCTGGTGTATG
GTCTGTTCTTTAGTTCAGTTTGTATCCCCTCAAAGCCATTATGTTGAATCCTAATCCCC
AAGGTGATGGCATTAAAGAAGTGGGCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTACCCCTTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTGCGCAAAACCCG
ACTCTGTCGTTGCTTGTATCTGAACTTCCAGCCTCCAGAACTATGAGAAATAAAATTCGG
TTGTTTGTAGCCTAA

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSGLVWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKFVFEGLLVLRCAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSAAPTTLNPAPQKSAAPGTAPEEAPGPLPPPTPSSDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

FIGURE 21

CCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGGGCCACCAGAAGTT
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
ATCTTACTGGGCTGCTACTCTTGGGGCACCCTAACAGTGGACACTTATGGCCGTCCCATCCT
GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAGGGGATGTGAATCTTCCCTGCACCTATG
ACCCCTCGAAGGCTACACCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAGTACCAGGGCCG
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCCTGGAGATGG
ATGACCGGAGCCACTACAGTGTGAAGTCACTGGCAGACTCCTGATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAA
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGGTTCTCCTCCCATCAGTTATATTGTGTATAAGCAACAGACTAATAACAGGAACCCATC
AAAGTAGCAACCCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
TTTCTGCACCTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
TTGAAGCAACATCTACAGTGAAGCAGTCTTGGGACTGGACCACTGACATGGATGGCTACCT
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTCCGAAGACATCCCAA
CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCTCTTCCATTTTTGACCCCGT
CCCTGCCCTCAATTTTGTATTCTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC
AATCCTAAGGCCGAGGCTTCAAGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
CTGAGGTTGTTTTGGCCCTCTGAACACAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCCTGGGTGGTAGGATCCTGATAATTAAATGGCAAGAATTGAGGCAGAAGGGTGGGA
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
CCAGTGTAGCCCACTTCCAGAACTCTGGGCAACAACTACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATGCCCAGATCAATGGCAACTACGCCCGCCTGTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTAAAAAATGCCCATTAGGC
CAGGATCTGTGACATAATTGCCTAGTCAGTCTTGCCTTCTGCAATGGCCTTCTTCCCTGTG
ACCTCTCTTCTGGATAGCCCAAAGTGTCCGCCCTACCAACACTGGAGCCGCTGGGAGTCACT
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCTCTCTAAATACCAGAGGGGAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCACTTTGGCATCTTGCCA
CCAGAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCGACTATATCAGGATCAT
TTCTCTTTCTTCAAGGCCAGACAGCTTTTAATTGAAATTGTTATTTTACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCTGGTGTCTCAATAAATATCTA
ATCATAACAGC

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCYDPLQGYTQVLVKWLVRGS
DPVTIFLRDSSGDHIQQAKYQRLHVSHKVPDVSLLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPIISYIWKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTMT
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAIILIISLCCMVFTMAYIMLCRKT
SQQEHVYEAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTGLTHTTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYVYQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 25

GTCGTTCCCTTGGCTCTCTCGCGCCAGTCCCTCCTCCCTGGTTCTCTCAGCCGCTGTGCGGAGGAGAGACCCCGGA
 GACGCGGGCTGCAGTCCGCGCGGCTTCTCCCGCCTCGGCGGCTCGCCGCTGGGCGAGTGTCTGAGCGCCCTAG
 AGCCTCCCTTGC CGCCTTCCCTCCTCTGCGCGGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCG
 CGCCGCGGAGCGCGGCTGGA TCGCGCGCTGGGCAGAAAGCAGCGCGCATTCAGCTGCCCCGCGCGCCCGGGCG
 CCCCCTGCGAGTCCCGGTTCCAGCCTGGGGACCTCTCCGAGCAGCAGCAACGCGCCTCGCCTCTGTCAGCGGCATC
 GCCCGCCGCGCCACAGCAGCATGATCGCGGGCTCCCTTCTCTGCTTGGATTCCCTTAGCAACCAACAGCTCAG
 CCAGAACAGAAAGCCTCGAATCTGATGACACATACCCCATCTTGACCGTGGCACCAGCGCAGGTGCTAACCTGT
 GACAAGTGTTCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCTCTGACAGCTTGGCCAT
 GTGGGGACCTTTACAGGCATGAGAAATGGCATAGAGAAATGCCATGACTGTAGTCTGAGCAGCTGCCCATGGCCATG
 ATTGAGAAATTAACCTGTGCTCGCTTGACTGACCGAGAATGCACCTTGCCACCTGCGCATGTGCTGCTTAAAGCT
 ACCTGTGCCCCCATACGGTGTGTCTGTGGGTGTGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
 GTTAAGCAGTGTGCTCGGGTACCTTCTCAGATGTGCCCTCTAGTGTGATGAAATGCAAAACATACACAGACTGT
 CTGAGTCAGAACCTGGTGTGATCAAGCGCGGGACCAAGGAGACAGACAAAGTCTGTGGCACATCCCGTCCCTTC
 TCCAGCTCCACCTCACTTCCCTCGGCACAGCCATCTTCCACGCGCTGAGCACATGGAAACCCATGAAGTCCCT
 TCCTCCACTTATGTTCCCAAAGGCATGAATCAACAGAAATCCAATCTTCTGCTCTGTTAGACCAAAGGTACTG
 AGTAGCATCCAGGAAGGGACAGCTCCGTGACAAACACAAGCTCAGCAAGGGGGGAGGAGCGTGAAACAGACCCCT
 CCAAACCTTTCAGGTAGTCAACACACAGCAAGGCCCCACACACAGACATCCTGAAGCTGTGCGCTGCTCAATGGAG
 GCCACTGGGGGCGAGAACTCCAGACGCCCATCAAGGGGCCCAAGAGGGAGACATCTAGACAGAACTACACAAG
 CATTTTGACATCAATGAGCATTGCGCTGGATGATTGTGCTTTTCTGCTGCTGTGCTGTGTGTGATTGTGGT
 TGCAGTATCCGGAAGACTCGAGGACTCTGAAAAGGGGCCCGCGCAGGATCCCAAGTGCATTGTGGAAGAGGCA
 GGGCTGAAGAAATCCATGACTCCAAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGTTATCGAT
 ATCCTGAAGCTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTACTGATTTCTTTGCAATCCGAGTGAG
 AGGGAGGTGTGCTGCTTCTCCAATGGGTACACAGCGCACACAGCGGGGCTACGCGCTCTGCGACACTGGACC
 ATCCGGGCGCCCGAGGCCAGCTCTGCCAGCTAATTAGCGCCTCGCGCAGCACCGGAGAAACGATTTGTGGAG
 AAGATTCGTGGCTGTATGGAAGACACACCCAGCTGGAACCTGACAACTAGCTCTCCCGATGAGCCCCAGCCCG
 CTTAGCCCCAGCCCCATCCCGAGCCCCAACCGGAACTTGAGAACTTCGCTCTCTGACGGTGGAGCCTTCCCA
 CAGGACAAGAACAGGGCTTCTCTGGAATGAGTCGGAGCCCCCTTCCCGCTGTGACTCTACATCCAGCGGCTCC
 TCCGCGCTGAGCAGGAACGGTTCTTTATTA CCAAGAAAAGAGGACACAGTGTGGCGAGGTACGCTGGAC
 CCCTGTGACTGACGCTATCTTTGATGACATGCTCCACTTTCTAAATCTGAGGAGCTGCGGGTGAATGAAGAG
 ATTCGCCAGGCTGAGGACAAACTAGACCGCTATTGCAAAATATTGGAGTCAGAGCCAGGAGCCAGCGCACACC
 CTCCTGGACTCTGTTTATGACCATCTCTGACCTGCTGTAGAACATAGGGATATGTCATTCTGGAAATTTACTCA
 ATTTAGTGGCAGGGTGGTTTAAATTTTCTCTGTTTCTGATTTTTGTGTTTGGGGTGTGTGTGTGTTGTGT
 GT
 TCTCTCTCTTTTGTTTTAAATTTTAAATTTTCTGTTTCTGATTTTTGTGTTTGGGGTGTGTGTGTGTGTGTGAA
 ATACCCACCACTAAAGTTTTTAAAGTTCATATTTTCTCCATTTTGGCTTCTATGTATTTTCAAGATATTTCTG
 TGCACCTTTAAATTTACTTAACTTACCAATAATGACAGTGTGACTTTTCCACACACTGATTTGTGAGGCTCTTAAC
 TTCTTAAAGATATAATGGCATCTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAAACCTACACACTCTTTT
 AAAAACCAATATATTAATCTATTTTATATTGTTTGTCTCTTATAAAATTTCTTAAAGATTAAAGAAATTTAAGA
 CCCCATTGAGTTACTGTAATGCAATCAACTTTGAGTTATCTTTAAATATGTCTGTATAGTTCATATTCATGG
 CTGAAACTTGACCACATATGTGCTGATTGTATGGTTTACCTGGACCCGCTGAGAAATGCTTGATTACTGTGAC
 TCTCTTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCTCAAGCCATCAGGATTTGTATTTAAAGTGCTT
 GACAACTGGGCCACCAAGAACTGAACTTCACTTTTAGGATTTGAGCTGTTCTGGAACACATTTGCTGCACTTT
 GGAAGTCAAAATCAAGTGCAGTGGCGCCTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTGTT
 TTTTATATACACATAATCAATAGGTCCAATCTGCTCAAGGCCCTGGTCTGGTGGGATTCCTTCAACAAAT
 ACTTTAAATTAAAAATGGCTGCAACTGTAAAGAACCTTGTCTGATATATTGCAACTATGCTCCCAATTACAAATG
 TACCTTCTAATGCTCAGTTGCCAGGTCCAATGCAAGGTGGCGTGACTCCCTTTGTGTGGGTGGGTTTGTGTG
 GTAGTGGTAGAGGACCGATACAGAAAAAGTCCCTCAAGTGTACTAAATTTATTAATAAACATGAGGTTTTGTGA
 AAAAAAAA

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNIGTYRHVDRATG
QVLTC DKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCWPWMIKLP
CAALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQGP HRRHIL
KL LPSMEATGGEKSSTPIKGPGRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYALQHW TIRGPEASLAQLISALRQHRRNDVVEKIRG
LMEDTTQLETDKLALPMSPLSPSPSPNAKLENSALLTVEPSQDKNKGFFVDESEPLL
RCDSTSSGSSALSRRNGSFITKEKKD TVLRQVRLDPCDLQIPFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEIIGVKSQEASQTLLDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTCCGTGGTGCCATCTACATTTTGGGA
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC
CATGGGGGAAAAATGATCCGCCCTGCCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTGGCC
TTGATGATTTGAAAATAAGTCTCTGTGACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCAC TGCTGCCATTGAAGTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGATTCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC
GAGTACCGCTGTGTCGGGGTGGTGGTCAGAAATGCCGTGCTCCAGGTGTTTACAGGCTGCTTC
TGGAAGACCATTGTCTCCGATGACTGGAAGGGTCACTACGCAATGTTGCTGTTGCCAAC
TGGGTTTTCCCAAGCTATGTGAGTTCAGATAAACCTCAGAGTGAGCTCGCTGGAGGGGCGAGTTC
CGGGAGGAGTTTTGTGCCATCGATCACCTCTTGCCAGATGCAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGATGTGCCCTTGCCACAGTGGTTACCTTGCAGTGCACAGCCT
GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAACATGTCCTTGCTCTCGCAG
TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGGTACCACTGTGCGGGGGCTCTGTCATCAC
GCCCCGTGGGATCATCTAGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA
CCATCCAGGTGGTCTAGTTTTCCCTGTTGGACAATCCAGCCCCATCCCACCTTGGTGGAAG
ATTGTCTACCA CAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAATGATCCAGCCTGTGTGCCCTGCCAACCTCTGAAGAGA
ACTTCCCCGATGGAAGAGTGTGCTGGACGT CAGGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCCTGTCTGAAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCCACAG
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACTGACGGGTGGCG
TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACCACTTTGGCATCGGCTGCGCAGAGGTGAACAAGCTGGGGTGTACAC
CCGTGTCACTCTCTTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCCGATCCTCCCCT
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCCTTGGAGCTCTGAGTTCGGGCACCA
GTAGCAGGCCCCGAAGAGGCCACCCCTTCCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTT
GTTTTTTGTTTTTTTGGAGGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTC AAGCGATTCTCTTGCTCAGCTTCCCCA
GTAGCTGGGACCACAGGTGCCCGCCACCACCCCACTAATTTTTGTATTTTGTAGTAGAGAC
AGGGTTTACCAATGTTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCTGCTT
CAGCCTCCCA CAGTGCTGGGATTACAGGCATGGGCCACCACGCCCTAGCCTCAGCCTCCTTTT
TGATCTTCACTAAGAA CAAAGAAGCAGCAACTTGCAAGGGCGGCTTTCCACTGGTCCAT
CTGGTTTTCTCTCCAGGCTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG
TGCAAGCCACCAACAGCCATCTAGAAAAGACGCCACAGCCAGAAAGTG CAGAACTGCAGTC
ACTGCACGTTTTTCATCTTAGGACCAGAAACCAACCCACCTTTCTACTTCCAAGACTTAT
TTTCATATGTGGGAGGTTAATCTAGGAATGACTCGTTTAAAGGCCTATTTTTCATGATTTCTT
TGTAGCATTTGGTGCTTGACGTATTATTGTCTTTGATTCCAATAATATGTTTCTTCCCT
CATGTCTGGCGTGTCTGCGTGGA CTGGTGACGTGAATCAAATCATCCACTGAAA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISFVAPDADAVAAQILSLLPLKFFPIIVIGIILILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVVRVGGQNAVLQVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVTAHHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFGYHLCGGSVIT
PLWIITAAHCVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPLISNKICNHR
DVYGGIISPSMLCAGYLTGGVDS CQGD SGGPLVCQERRLWKLVGATSF GIGCAEVNKP G VYT
RVT SF LDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

FIGURE 29

CCCACGCGTCCGTCCTAGTCCCGGGGCCAACTCGGACAGTTTGCTCATTATTATGCAACGGTCAAGGCTGGCTTGT
GCCAGAACGGCGCGCGCGCGCGCACGACGCGACACACACGCGGGGAAACCTTTTAAAAAATGAAAGGCTAGAAGA
GCTCAGCGCGCGCGCGCGCGCTCGCGGAGGGCTCCGAGAGCTGACTCGCGAGGCGAGGAATCCTCCGGTGCGGA
CGCCCGCGCCCGGCTCGGCGCCCGCGTGGGATGGTGCAGCGCTCGCCCGCGGGCCGAGAGCTGCTGCACCTGAAG
GCCGCGCACGCTGACGAGCGCGCCGCTGCCCCGTGTCCCCCGCCCGCGCCCTCTCGCTCGCCCTGGCCCGGTGCT
GCTCGCGCCCTGGCAGGCGCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTTCAGTGCCTCTGT
TCGGAGTGGGAGCCTCTGGATCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGTGTAATATTCGACT
ACAAACGGGAAAGCAAGAACTGATCAAAATCTGGAAAGAAATGAAGCTCTCATTCGCCAGAGTTTCACGGAAAC
CCCACTATCTGCAAGCGGTACTGATGTCTCCCTCGCTCGAAATTTACCGGTCACCTGTTATCCACCCACCTCTCAGAC
ACGGGGATATTCTGATTTCAGCACTCAGTCTCAGCACGTTCTGCTGTCTCAGGGGACTTATTGTGCTTGAATAAT
AAGCTATGTTCTTAGAACCAATGAAAGTGCAACCAACAGATACAACTCTTCCACGCGAAGAGCTGAAAGCGT
CCGGGGATCATGTGGATCACATCAACACACCAAACTCGCTGCAAGAGATTTGTTTCCACCCACCTCTCAGAC
ATGGGCAAGAGGCATAAAAGAGAGACCTCAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCG
AGAGTTTCAGAGGCCAAGGAAAGATCTGGAAAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCACGTTGACAA
GTTTTCAGAGCACTGAAACATTCCGGATCGTGTGTGTAAGCGTGGGAAGTGTGGAATGACATGGACAAATGCTCTGT
AAGTCAGGACCCATTCAACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAATCCGA
TGCAATGCGCAGCTTGTGAGTGGGGTTTATTTCCAGGGGACCAATCGGCATGGCCCCCAATCATGAGCATGTG
CACGGCAGACAGCTGTGGGGAAATTTGATGGACCATTCAGACAATCCCCCTTGGTCAGCCGTGACCTGGGCACA
TGAGCTGGGCCACAATTTCCGGGATGAATCATGACACATCGGACAGGGCTGTAGCTGTCAAATGGCGGTTAGAA
AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTCCCATGTGTGTTGAGCAGTTGCGACAGGAAGAGCT
GGAGACCAAGCTGGAGAAAGGAATGGGGGTGTGCTGTTAACTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCA
GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
CTGCAATGCAACCACTGTACCTGAAGCGGACGCTGTGTGCGACATGGGCTGTGCTGTGAAGACTGCCAGCT
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGCCC
TCACCTGCCAGCCAATGTGTAACCTGCAGATGGGCACATCATGTGAGGATGTGACGGCTACTGTCAATGGCAT
GAGAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA
GAGAGTCAATTTCTCAGGTGATCCTTATGGCACTGTGGCAAAGTCTCGAAGAGTTCCTTTGCCAAATGCGAGAT
GAGAGATCTAAATGTGGAAAAATCCAGTGTCAAGGAGGTGCGAGCGGGCAGTCATTGGTACCAATGCCGTTTC
CATGAAGAACAAACATCCCTCTGCAGCAAGGAGGCGGATCTGTGCGGGGGACCAAGCTGTACTTGGGCGATGA
CATGCCGACCCAGGGCTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCTGAATCGTCAATGTCA
AAATATTAGTGTCTTTGGGTTTCAGAGTGTGCAATGCAAGTGCACGCGGAGGAGGCTGTGCAACACAGGAAGAA
CTGCCACTCGAGGCCCACTGGCACCTCCCTTCTGTGACAAGTTTGCTTTGGAGGAAGCAGACAGCAGCGGCC
CATCCGGCAGCAGAAAGCAGGCAAGCTGCAGATCCAAAGGAGCGCGGCTCAGGGCCAGGAGCCCGGTGGG
ATCGCAGGAGCATGCTCTACTGCTCTACTGACATCTATCTGAGCCCTCCATGAGAGCTGAGCTGTGGCTTTGCCATGTT
CTGCTGCAGAGGAGTCAAGCTGCCCCCAAGGCTCTCTGTGACTGGCAGCATTAATCTGTGGCTTTGCCATGTT
TCCATGACAAACAGACACAAACAGATTCTCGGGGCTCAGGAGGGGAGTGCATTAAGTCTGGCCTTTGAG
CAGTGCAGGAAGGGCAGCGACTCTCTGTTGAGCTTCTGCTAAAAATGAGACATGCTTCAGTGTCTGCTCTTGA
AGATAGCAGGTTTACCACTCTGGCAGGCCCCAGCCCTCGACGAAAGGAGAGGACTCAAAGTCTGGCCTTTG
ACTGAGCCTTCAACAGAGTGGGGGAGAGCAAGGGTTGGGCCAGGTGCCCCCTTCCCGAGTGACACTCAGCCT
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTATGACTTTATATAGAAAT
AGCAGGTTTGTATTGTTTAAATTTATCAGAGAGCTGCCACCTTCCATCTCCATCAAAGCAAGTGAATGCAAC
TGAAACAACTGGAGAAGAGGTAGGAGAAGGGCGGTGAATCTGGCTCTTGGCTGGACATGCTGTACCCAGC
AGTACTCAGGTTTGAAGGTTTGCAGAAAGCCAGGGAACCCACAGATCAACAACTCTTATTAACAAAGTAGAA
TGTTAAAAAGTGAAAAATGTAAAGAGCTAACTCCATCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT
GAAAT

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIPVKSFDSK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLPAPAKKLKSVRGSCGSHHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDFK
YRPLNIRIVLVGVEVWMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDITLDGCSCQMAVEK
GGCINMASTGYPPPMVFSSCSRKDETSLEKGMGVCLFNLPEVRESFGGQKCGNRPFVEEGEE
CDCGEPEECMNRCNATTC'CLKPDAVCAHGLCCEDCQLKPAGTACRDSNSCDLPEFCTGAS
PHCPANVYLHDGHSQDQVDGYCYNGICQTHEQQCVTLWGPAGKAPAGICFERVNSAGDPYGN
CGKVSXSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQGGRIICRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRCQCNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDSGPIRQAEARQEAESNRERGQGEFVGSQEHASTASLTLI

Signal peptide:

amino acids 1-28

FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTGGGGGTT CAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGCAGGANTTCTTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCTCTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

[illegible]

CATCTCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTGATTTTGTGTAGAGATGGGA
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCGCCTCGGCCCTCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCGGCCACAACTTTTAAAGAGTTAAT
GAAACCATACCTTTTACATTTTAAATGACAGGAAATGCTCACAATAATTGTTAAACCCAAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAAA
TACCAAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA
CTTTTAACAAAAAAATTTGCATCACTTTTAAAGAACAGAAAAATTTCTGAAGGTCATATGGG
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTGAAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTCTAAGCAACTTAAATGTTTTGTTTCGA
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCCCTACTTGCTATCTCCCTGCACGACGAGGACGAGCCACCCATCCTCCAG
ACTCATGAGCAGCAGCTGGACACACGCGACTGACTCCTCAAAATGGGTGAAGGGATGGTGCGGA
TGCTCATTCTGGGTCTGGACTACTCTGGCGCTGCTCTCACTCCGTGCGAGGTTTCTTCAATTTGTT
CCTTTAACAGTATGCGGAAGCTACTGCAGCGGAAACCACAAAGCCCTCCAACAGTGCCCT
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAACCGAATCCTAAATGGTGCTT
AGAAGTTCATGTGGCAAGGAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCATAGGCCGCGGATCACCTG
AGGTCAAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATTGACTGGGCGTGGTGGTGAGTGCCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAGCCAAAGTGCAAGTGAGT
CACGCCTGTAATCCCGGCACCTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA
AGACCATCCTGGCTAATACAGTGAAACCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCAGCTACTCGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGGCGAGGCTGTCAGTGCAGCGGATTTGCGCTACTGCACTCCAGCCTGGGCGCAG
CGCGAGACTCCGTCTCAAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL
LHLYH

Signal peptide:

amino acids 15-27

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Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	

[illegible]

FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHG IQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPTLKLFPQGQEA VKYQGPRDFQTLNWMQLTNEEPVTPEPEVEPPSAPE
LKQGLYELSASN FELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRD GKKVDQYKGRDLES LREYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFD DTTAEGITFIKFPYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

Signal sequence:

amino acids 1-32

FIGURE 36

CTTTTCTGAGGAACCAACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCTGCAGGATTCCG
GGTGGAAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTTCGGGTGTTCAATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTTGCTATTTTCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAA

FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQISLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEEG
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKEKGLLGIPGEKGKAGTVCDGRY
RKFBVGQLDISIARLKTSMKFVKNVIAIGIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQYNSNWNNEGEPSDPYGHEDC
VEMLSSGRWNDECHLTMYFVCEFIKKKK

Signal peptide:

amino acids 1-25

FIGURE 38

GGTTCTATCGATTTCGAATTTCGGCCACACTGGCCGGATCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCTGCTCTCCGCCGCTGTGGAGTGGTGGGGCCCTGGGTGGGAATGGCGGTGT
GCCAGCGCACCGCGCGCTCCCTGGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTT
CGGAAGGGAGGATCAGGGATGTTTTCGAGCGGCTGGAACACAGACGGTCCGATAGAGGAAGC
GGGCTCCATGGCTGCCCTCTGTCTGCTGCCCTGCTGCTGTTGTACCGCTGCTGCTGTGA
AGCTACACCTCTGGCCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTCGCGCCGACCCGGAAGG
TCCCGAGGGGGGCTCGAGCTGGCCTGGCGCTCGCGGAAGTGGCCCGAGCGCGCCGCGCG
ACACCTTTCTCATTACCGGCTCGCGGCTTTAGCTACTCAGAGCGGAGCGCGAGATTAAC
AGGGCTGCACGCGCCTTCTTACGTGCGCTAGGCTGGGACCGGACCGCGCGACAG
CGCGAGGGGAGCGCTGGGAGAAGCGAGCGGCGAGCGCCGGAGCCGGAGATGCAGCGCGCG
GAAGCGGCGCGAGTTTTCGCGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCGCGCCGCT
CTGTACCTGGAGCACTGTGGCGCTGCTCCTCCCGCTGGCCAGAGTTTCTGTGGCTCTG
GTTGGGCTGGCCAAGCGCGCCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCC
CCTTGCTGCACCTGCCTCCGCGAGCTGCGCGCGCGCGCGCTGGTGTGGCGCCAGAGTTTCTG
GAGTCCCTGGAGCGCGACCTTGCCTCGCTGAGAGCCATGGGGCTCCACCTGTGGGTGCGAGG
CCCAGGAACCCACCCTGCTGGAAATTAGCGATTGTGCTGGCTGAAGTGTCCGTTGAAGTGGAT
GGCCAGTGCCAGGATACCTCTTCTCCCCCAGAGCATAACAGACACGTGCCGTGTACATCTTC
ACCTCTGGCACCACGGGCTCCCCAAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTGCCTCCAC
TCTACCACATGTCCGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG
GTGCTGAAATCCAAGTTCTCGGCTGGTCACTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCGCCCGAGCAAGGCAG
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCGAGCGGGCTGCGCCAGATACCTGGGAGCGT
TTTGTGCGGCGCTTCGGGCCCTGCAAGTGTCTGGAGACATATGGAATGCAGAGGGCAAGCT
GGCCACCATCACTACACAGGACAGCGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGC
ATATCTTCCCCCTTCTCTTGATTGCTATGATGTCAACACAGGAGAGCCAATTCCGGACCCC
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGTGGTGGCCCCGGTAAGCCA
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCAGGGGAAGTTGCTAAAGG
ATGCTTCCGGCTCGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC
CACAAACGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTTCTTCAGGAGGTGAACGTCTATG
GAGTCACTGTGCCAGGCGATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTTCTGCGTCCCCC
CACGCTTTGAGCCTTATGCACTCTACACCCACGTGTCTGAGAACTTGCACCTTATGCCCG
GCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAACAGCAGAAAG
TTCGATGGCAAAATGAGGGCTTCGACCCAGCACCTGTCTGACCCACTGTACGTTCTGGAC
CAGGCTGTAGGTGCCCTACCTGCCCTCACAACCTGCCCGGTACAGCGCCCTCTGGCAGGAAA
CCTTCGAATCTGAAGAACTCCACACTGAGGCACCTGAGAGGAACTCTGTGGGTGGGG
CCGTTGCAGGTGTACTGGGCTGTGAGGACTTTTCTATACAGAACTGCGGTCACTATTTT
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTGACCTAAAAAAGGATAACAGGGTAATAAGC
AAAAAAGGCGCGCGCACTCTAGATCGACCTGCACTGAGGATAACAGGGTAATAAGC
TTGGCCGCATGGCCCACTTGTTATTGAC

FIGURE 39

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913
><subunit 1 of 1, 730 aa, 1 stop
><MW: 78644, pI: 7.65, NX(S/T): 2
MGVCQQRTRAPWKEKSQLERAAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPL
LLLKLHLWLPQLRWLPADLAFVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRFRFSYSEAEERESNRARAFLRALGWDWGPDDGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGVPVGYLSSPQSITDTCLYIFTS GTTG LPKAARISHL KILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVPQYIGELCRYLVNQPP
SKAERGHKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW
LYKHIFPFSLIRYDVTITGEPIRD PQGHC MATSPGEPGLLVAPVSQQSPFLGYAGGP ELAQGK
LLKDVFRPGDVFNTGDDLVCDDQGF LRFH DRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRP PHALDLMQLYTHVSENLPFYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLS DPLYVLDQAVGAYLPLTTARYSALLAGNLRI
```

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

[illegible]

CTTGTGTTTAAGCTGAACTTTCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA
 GATCTCCCAAGAACCTTCGAGCTACACCAACAGACACAGCGCGCATACACACTCGCTCTC
 CGTTGTTCATCTCCCTCCGGGGGAGCGCGCGCTCCACCTTTGCCGACACTCGCG
 GAGCGGAGCCCGCAGGCTCTCAGGATTTGCGCGCTCGGAATCTCGGATTCGAGCTCTGAAACCC
 CCATGGTGGTTTTTAAACACTCTCTTTCTCTCTCTCTGTTTGAATGTCACGTTTCCA
 TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCAGCCAGCCCTTGTGGCTTGCCATCGT
 CCATCTGGCTTTATAAAGTTTCTGAGCGCAGTCCAGAGGGCTGCGCTGCTGCTGCCCTCGG
 CTGGCAGAAGGGGTGACGCTGGGCAGCGCGGAGGAGCGCGCGCTGCTCTGGCGGGCTT
 CGGCTTTGAGGGGCAGAGTGAAGAGCGCACCGGCCGTGGGGTTTACCAGACTGGAAATTTGATG
 TTGACCACATGCCCTTTGGGATCGGGGCTGGAATCTCCCTCTTGGGGCTGCTGCTCTCC
 TCCCGCGGGGGCGGATGTGAAGGCTCGGAGCTCGGAGAGTGCBCGAGCGTACGTTGCC
 AAGGGATTCAGCTCGCGGCATCCCTACACGAGGATCGCAGGGGAACCTTAAGAATCTG
 TCCTCAGGAATATACGTCTGCACCAAGAATAAGGAACAAGTTAAGCCAAACAAGCAAC
 TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG
 CATAAGAATTTGACGAATTTTCCGAGAGCTCTGGAGAATTCGAGAAAGACTCATAATGAT
 TATGTTGTACCGACATATGCGATCTGTACATCAGAATTCAGAAGTCTTCACGAGCTCT
 TCCAGAGCTGCAAAAGGTACTACTGCGGGTAAATGTGAATCTGGAGGAATGTCAATGAC
 TTTTGGGCTCGGCTCTCGGAACGGATGTTTTCAGCTGATAAACCTTCAGTACACTCGTCA
 AGACTACTCTGGAATGTGTGAGCAATACTGACCACTCAAGCCATTGGAGACGTGGCCCC
 GGAATCGAAGATTCAGGTTACCCGCGCTTCATTGTGTCGAGGACCTTTGTCCAGGGGCTG
 ACTGTGGGCAGAGAAGTTGCAAAACGAGTTTCAAGGTGAGCCAAACCCAGGGTGTATCCG
 GGCCTCATGAAGATGCTGTATGCCCATACTGTGCGGGGCTTCCACTGTGAGGCCCTGCA
 ACACTACTGTCTACAGCTCAGTAAGGGCGCTGTGGCAATCAGGCTGACCTGCAGCAGAG
 TGGAAATGTTTATAGATCGAATGCTCTTGGTGGCAGAGCGCATGGAGGGGCCATTCAACAT
 TGAGTCGGTCTGAGCCAGCATAGATGTCAAGATTTCAAGACCATTAACATCGAAGAA
 ACAGATCTCAGGTTGTCTGCAAAAGTCTTTCAGGATGTGGTCAAGCCAAACCTGCTCGAGCC
 CTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATACAGTTTCAGGCCCTACAATCTGGA
 GGAAGAACCAACAACCTGCTGAGGACAAGCTTGACCGGGTGTGCACAGACATAAAAGAGA
 AATTGAAGCTCTCTAAAAGGTTCTGTGTGACATTACCTACTACTTCGAAGGACAGAGC
 GTGACAGCGGGCACGTCCAACGAGGAGGAATGTGGAACGGGCACAGCAAGACAGATACCT
 GCCTGAGCTCATGATATGGCTACCAACAGATCAACAATCCGAGGTGGATGTGGACA
 TCACTCGGCCGTGACACTTTTCATCAGACGAGCAATTATGGCTCTCCGTTGTATGACCAACAA
 CTAATAAAGCGCTTACATGGCAATGATGTAATTTCCAGGACAAGTGAATGAATCCAGTGG
 CTCAGGAGTGGCAGTGGGTGCATGTGATGACGTGTGCCAGGAGTTGAGTTTGTTCACCA
 CAGAGGCCCCCGCAGTGGATCCGACCGGAGAGAGGTGGAATCTTCTGACGCCACAGCGTGGC
 CACTCCCTGCTCTCTGGTCTCTCACTGTCATTGTCTGGCATCTGGCAGACTGTGCAGATA
ATCTTGGGTTTTTGGTCAGATGAATCGAATTTAGCTATCGAATGGCCAACTCACTCTT
 TTTCTACACTCTGGACATGGACATGCCACAAAACCTACCGTTTCTATGAGAAGAGAG
 CAGTAATGCAATCGAATCCCTTTTTGTTTTTCCAAAGAGTACCGGGTGCAGACTGAACGT
 CTTCCTCTTTCTTCAGCTATCTGTGGGACCTTGTTTATTCTAGAGAGAATTTTACTCAA
 ATTTTCTGTAACGAGGAGATTTCTTACCTCTATTGCTTTTATGCTGACAGAGATAAGGAAT
 CTCAGTTGTGAGGGTTTTTTTTCTTCAATTTTAAAT

FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKARSCGEVRQAYGAKGFSLADIPYQETIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF
VRTYGMLYMQNSEVFQDLFTTELKRYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY
LECVSKYTDQLKPFQDVPRKLIKQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNQENSMQVSAKVFQCGGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTEFEFVTTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCGAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAAACGCACG
 CAGTTTGCAGCGCCTGCGCGCGGTGCGCCAACTACGCAAAAGCAAGCGGGCTCGCGCGGACCGCGCGCGGGGC
 TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT
 GGAGGGAGATCAGGAAACGGCTTCTTCTCCTCAGTCTCGCCGCTGTTGAGTGTGCGGGAGATTGGCAAAACGCCTAGG
 AAAGGACTGGGAAAAATAGCCCTGGGAAAGTGGAAAGGTGATCAGGAGGCCGGTCCACTACGCGCAGTTTATCTG
 TCTGATCAGAGCGCAGCGCAGCGCTCCACTTCGCAAGTCTTTCAGGTGTGGGACCGCAGGACAGACGCGCGCA
 TCCCGCCGCCCTTCGTACCAAGCTCCAGGAGAGTCAGCGCTCGCTCCCAACGTCAGAGGCGCTCTGGCCACGA
 AAAGTTCCTGTCCACTGTGATTCTCAATCCITGCTTGGTTTTTTTCTCAGAGAACTTTTGGGTGGAGATATTA
 ACTTTTTTCTTTTTTTTTTCTTGTGGAAGCTGCTTAGGGAGGGGGAGGAGGAGGAGAAAGTGAATGTGC
 TGGAGAAGAGCGAGCCCTCCTTGTCTTTCGAGTCCATCCATTAAAGCCATCACTTCTGGAAGATTAAAGTTGT
 CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTCTTGCCAGGTGGAGAGTCTTCAACCTCTGTTGGGTGCTG
 TGTGCGCCCGCAGCGCGCGGGGCGCGTGGTCTCGCGGTGGAGTCTCACCTGGGACCTGAGTGAATGGTCCCA
 GGGCTGTGCGGGCATCCGCTTCGCTCTCCACAGGCTGTGTCTGCTCTGGAAAGATGCTAGCAATGGGG
 CGTGGCAGGATTCTGGATCCTCTGCTCTCACTTATGGTTACCTGTCTGGGGCCAGGCCCTTAGAAGAGGAGG
 AAGAAGGGGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACTCCACTCCAGGCCCATCTCA
 TTTTCATCCTAGCGGATGATCAGGGATTAGAGATGTGGGTACACCGGATCTGAGATTAAACACCTACTCTTG
 ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTTCACACCTCCAGGAGTCACT
 TTATTACTGGAAGATCAGATACACACCGGACTTCAACAATTCTATCATAGACCTACCCACCCCACTGTTTAC
 CTATTGGACAAATGCCACCTTACCTCAGAACTGAAGGAGTTGGATATTCAACGCATATGGTGGGAAATGGCACT
 TGGGTTTTAAAGAGAAAGATGCTGCCACCAAGAGAGGATTGATACCTTTTTTGGTCTCCCTTTGGGAAAGTG
 GGGATTACTATACACTACAAATGTGACAGTCTTGGGATGTGTGGCTATGACTTGTATGAAACGACAATGCTG
 CCTGGGACTATGACAAATGGCATATATCTCCACAGATGTACTCAGAGAGTACAGCAAACTTGTAGCTTCCATA
 ACCCCACAAAGCCTATATTTTATATACTGCTATCAAGCTGTTCACTCACCAGTCAAGCTCCTGGCAGGTATT
 TCGAACACTACCGATCCATTATCAACATAAAGAGGAGATATGCTGCCATGCTTCTGCTTAGATGAAGCAA
 TCAACAAGTGAACATTGGCTCTAAAGACTTATGGTTTCTATAAACAAGCATTATCATTTACTTCTCAGATAATG
 GTGCCAGCCTACCGCAGGAGGAGTAAGTGGCTCTCAGAGGTAGCAAGGAACATATTGGGAAGGAGGATCC
 GGGCTGTAGGCTTTTGTGATAGCCCACTTCTGAAAAACAAGGAAACAGTGTGTAAAGAACTTGTGCACATCACTG
 ACTGGTACCCCACTCTCAITTTCACTGGCTGAAGGACAGATTGATGAGGACATCAACTAGCTGTATGATATTG
 GGGAGACCATAAGTGAGGCTCTCGCTCACCCGAGTAGATATTTGACATAACATTGACCCCTATACACCAAGGC
 AAAAAATGCTCCTGGGAGCAGGCTATGGGATCTGGAACTGCAATCCAGTCAGCCATCAGATGTCAGCACTG
 GAAATGTCTTACAGGAAATCCTGGCTACAGGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG
 GTGCGCAATGAACGGATCACCTTGTCACTGGCAAAAGTGTATGGCTTTCAACTCAGCGGACCCGATATGA
 GAGGGTGGACCTATCTAAAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCAGATTCAACAAAAC
 TGCAGTGCGGTGAGGTATCCCCCAAAGACCCAGAAAGTAACCTTAGGCTCAATGGAGGGGTCTGGGACCATG
 GTATAAAGAGGAAACCAAGAAAGAGCCAGCAAAAACTAGGCTGAGAAAAAGCAAAAGAAAGCAAAAAAA
 GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAACACGAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
 GGCCTGTCTTTCATGCTGTGCCACTCAGAGACTTCTGCCACCTGGCCGCCACACTGAAAACTGTCTCCTGCTCAGTG
 CCAAGGTGCTACTCTTGAAGCCACACTTAGAGAGAGTGAGAGATGTTATTCTCTCGCTCCTTTAGAAAAAGTGTG
 GTGAGTCTGTGATCTCACTGTGTGCTTCACTGACCAAACTGCTTTGAATATAGAGGAGGAGAACATA
 ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAACTACCTTTGATAAATTAC

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

[illegible][illegible]

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAQHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYHGSEIKTPTLDKLAEBGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGVKGWHLGFNRKEC
MPTRRGFDFTFFGSLLGSGDYIYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA
LKYGYFYNNSIIYSSDNGGQPTAGGSNWPLRGSKGYWEGGIRAVGFVHSPLLKNKGTVCCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECTGNCLQEILATATGSPLSLSATWDRGTGGTMNGSPCQLAKVYGFSS
TSQPTHMARGWYTLGTIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGCT
TTAGCTGCTACGCGGGTCCGGCCGGCGCCCTCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGAATGCTCTGCCCCCTGGAGCCTTGCCTCCCCGTGCTGCTCTCCTGGGTGGGAG
GTGGTTTCGGGAACGCGGCCAGTGC AAGGCATCACGGGTTGTTAGCATCGGCACGTGAGCCT
GGGGTCTGTCACTATGGAACATAAAGTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCCTGGGACCAACAAAT
GCAGATGCTTTCCAGGATACACCGGAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGCCATGCTCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCTCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAATCTAGGACATGTGCCATGATAA
ACTGTGAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCTTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTGGAAGCTACTACTGCAAAATGT CACA
TTGGTTTCGAAGTGC AATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCCTCAAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG
TGAAGGAAGTCTCAGAGCAGCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAGGCAAAAAATTAAAAATGTTACCCGAGAACCACAGGACTCC
TACCCCTAAGGTGAACCTGACGCCCCCTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAC
CTCATGGAGGTAAAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAAGAG
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCT
AAGGTGAATGAAGCAGGTGAATTCCGCCCTGATTTCTGGTCCAAAGGAAAGCGCTAAGTCCAA
ACTGGAACATAAAGATTTAAATATCTCGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAACAGGATAGAGAAGATGATTTTGACTGGAATCTCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTTCCGGCCTTGGCAGGT CACAAGAAAGACATTGGCCGATGAAACTTCT
CCTACCTGACCTGC AACCCTCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGGAAACTTCAGTGTGTTGTGAAAAACAGTAACATGCCCCGGCATGGGAGAAAG
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAAATTCAAGTGTATCAAGGAACATGATGC
TACCAAAAGCATCAATTTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCGAAATCGCAGTGG
ATGGCGTCTTGCTGTTTTCAGGCTTATGTCCAGATAGCCTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTTGACTTTGTATGTGAGTTCCTCGGTTTTTTTGATATTGCATCATAG
GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTTATG
TAAAGATGCTTTCTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCAGTATCT
TCTCAGTCATTTCTGAATCTTTCCNCATTATATATAAATTTGGAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA
GAAAAATAGAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGA
AAGTATGATCATCAAGATAGACTTTTGCTTAAGTGGCTTAGCTGGGCTTTTCATAGCCAAAC
TTGTATATTTAATCTTTGTAATAATAA

FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGPNNKRCFFGYTGKTCSDVNECGMKPRPCQHRCVNTHGSKYKFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVI CP
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPPTPK
VNLPFPNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGGCTGTCGCGCGTCTCTCTGCTCTTGGTGCAGCTGCTG
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCC
AGAATGGGAGCTGACTGATATGTTGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTCAGCCAGAAGAGTGCAT
GAGCTGGAAGGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAAATGTCCAGCGTTCTCTGTGC
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTCTC
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTTAAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATGTGGAGAATTCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCAAGATGACAACCAAGTCTGTGTGTCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTGTGATTTT
ACTTTTAAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG
ATTGCCATGAATCTTGCAAAA

FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343
><subunit 1 of 1, 289 aa, 1 stop
><MW: 32268, pI: 9.21, NX(S/T): 0
MVVVVTGASSGIGBELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSLCMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQCKIVTVNSILGIIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIIVSNICPGP
VQSNIVENSLAGEVTTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW
QYMPITWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

FIGURE 48

GCAGCTGGGCACCGCCATCAGCTGTTGCGCGTCTTCTCCTCCAGGTGGGGCAGGGTTTC
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCCGG
TTGCTCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCCTCTGTCC
TGATGCTGCTGAGCTCCCTGGTGTCTTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTGTT
TTCGTGCTCTATGATTTCTGCATTGTTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
GTGGCTCAGTTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACCTGAGCCCTCA
ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCTCTGTG
GACAGCGTGGCCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCCC
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
CTGGGTCTCTCACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAATGAATTCTGGT
CAGTGGTCTTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
GCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
GCAGCTCGCCACCCACGACCCACACACCCCTCTGCTGCCCCAGCCCGCCCATGCTTCC
CCTTTGGAGCCTCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACGTGATCTACAACCAAGCT
GCACCAGCGACACCTGTCCAACCCGGCCCCGGCTGGGATGCTATGTGGGGGCCCCAGCCTG
GGGTGCAGGGCCCTGTCAAGGAGATTCCGGGGGCCCTGTGCTGTGCCCTCGAGCCTGACGGA
CACTGGGTTCAGGCTGGCATCATCAGCTTTGTCATCAAGCTGTGCCCAGGAGGACGCTCCTGT
GCTGTGACCAACACAGCTGCTCAGGTTCTTGGCTGCAGGCTCGAGTTCAAGGGGCAGCTT
TCCTGGCCCCAGAGCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGTA
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCCTCCCATGGCCCTGGGAGGCCAGGCT
GATGCACCAAGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTG
CTGCCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA
CCGGAGGAGTGGGGCTGAAGCAGCTCATCTGTCATGGAGCCTACACCACCCCTGAGGGGGG
CTACGACATGGCCCTCTGTGCTGCTGCCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
TCTGCTGCCCCATCTCTGACCACCACTGCTGCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
GCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCCTCCTGGGGCCTAG
GGCCTGCAGCCCGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCGCGGGGATGG
TGTGTACCACTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCACCCTGCTG
CATGAGGTGAGGGGCACATGGTTCTTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG
CCCCGCCAGGCCGGCGGTCTTCAACCGCGTCTCCTGGCCTATGAGGACTGGGTGACAGTTTGG
ACTGCGAGGTCTACTTCGCCGAGGAACAGAGAGCCGAGGCTGAGCCTGGAAGCTGCCTGGCC
AACATAAGCCAAACCAACCAAGCTGTGAAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
AGGCAGGCCAAATGGCATTACTGCCCTGTCTCTCCCAACCCTGTGATGTGTGATTCCAGGCAC
CAGGGCAGGCCCAAGAAGCCAGCAGCTGTGGGAAGGAACCTGCTGGGGCCACAGGTGCCCA
CTCCCCACCTGCGAGGACAGGGGTGTCTGTGGACACTCCCAACCCAACTCTGCTACCAAGC
AGCGCTCAGCTTCTCTCTCTTACTCTTTTTCAGATACAATCAGCCAGCCACGTTGTTTT
TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTAACTTAAATAAATTTGTTAC
AAAAATAAA

FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571
MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITYAINVSLMWLSFRKVPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDIALLLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPAPRPGMLCGGPQPGVQGPCGDSGGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPGAGISSLQTVPTLLGPRACSR LH AAPGGDGSPILPGMVCTSAVGELPSC EGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCCCGCCCCCATT CGGGCCGGGCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCAGAGTCCGGCGCGGCGGCGGAGGGGAGCCTTCCACCACGGGGAG
CCCAGCTGTACAGCCGCTCACAGGAAGATGCTGCGTCGGCGGGGCGAGCCCTGGCATGGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCTGTGCTGCTCCTTCTCC
CCTGAGCCTGGCTTACGCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATAACCAACA
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC
TCTTCCCGACCTGTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCTGCGTGTGGCG
GACGAGGGCAGCTTACCTGCTTCGTGAGCATCCGGGATTTTCGGCAGCGCTGCCGTGAGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTT
TGGCAGGATGGGCAGGGTGTGCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA
GCAGGGCTTGTTTGATGTGCACAGCGTCTGCGGGTGGTGTCTGGGTGCGAATGGCACCTACA
GCTGCCTGGTGCAGCAACCCCGTGTGCAGCAGGATGCGCACRGTCTGTCCACCATCACAGGG
CAGCCTATGACATTTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTTCTGTGTCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAAGAAGATGATGGACAAGAAATAGCCTTGACCATGAGGACCAGG
GAGCTGTACCCCTCCCTACAGCTCCTACCCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCGTTCTCCAAGGATGCGATACAC
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCCTTT
TTCTTATAGACACAATGAACAGACACCCACAACCTTAGTTCTCTAAGTCATCCTGCCCTGCT
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCAACCTC
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCCTTTTTTCTCCAAAGATGCAATATTGAGA
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCCCTGTTC
TCCAATGGCCGTGATACACTAGTGATCATGTTGAGCCCTGCTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGCAGGTGCGGCCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCCTTC
CCCTCCTTCTCTCCCTGCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCACCACCATGGTGTCTATTCTGGGGCTGGGGCAGTCTTTTCTGGC
TTGCCCTGCGGCAGCTCCTGGCCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG
GATGTCATCTCTCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTGTAAACTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAA
AAAAAAAAAAAAA

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALVQVPEDFVVALVGTDLCCSFSPPEGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASRLQRVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDQGQVPL
TGNVTTSQMANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGESEKLTALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

FIGURE 52

TTCTGTGACCCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
CTGAACCTTGCTCTGAAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTTCCTTGCTTCAGACAACATGAGGCTTTTCT
TGTGGAAACGGGCTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC
ACAAAACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGGACCAGGGCTTGAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTTCTCTCTGC
TCTGGGCTATGAAAAAGAAGGAAAAGGTAATAATCCCCAGAAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTGAAAATGGACCAAGATCCCATGAATCATTCAGAAGAAATGGATCTT
AATGATGACTGGAACCTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGA
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGTATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCCTTTAATAATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTATACAATGTTCTTTCTTGCTTTGTTTTTATTTTATATATTTTTT
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTTCACAG
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAAGTGTGCAACTGGGAATATACC
ACGACATGAGACCGGTTATAGCACAAAATAGCACCTTATATTTCTGCTTCCCTCTATTTTC
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTTCAT
GTTATAATGAATAGTTTATGTGTAACCTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA
TGTTTGTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAAAACAAGGTTAAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAAGCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGCGTGGTGTATGCGCTGCTGTAATCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAAATCACTTGAACCCGAGGCGAGGTTGCGGTAAGCCGAG
ATCACCTNACGCCCTGGACACTCTGTCTCGAAAAAAGAAAAAGAACACGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGCTCTCTAGTGAT
TGGTGGCCTATTATGATAAATAGGACAAATCATTATGTGTGAGTTTCTTTGTAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAGTTATATTTATATTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACACTACAATAACA
TTGTATCATAGAATAAAGTAGTAAACAGCTCTACATTTTCCCATTTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCTGTAATCCAGCACTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA
CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGACACCTGTAGTCCCAGCTACTCGGGAG
GCTGAGACAGGAGATTTGGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAAGATTGTGCC
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGAGCAGA
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATT

FIGURE 53

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
MRLFLWNAVLTLFVTSLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSIL
FHSTHKHNNGQPIWFTTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKKGAVVNESHHDALVED
IFDKEDDKDGFISAREFTYKHDEL
```

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

FIGURE 54

AATAAAGCTTCCTTAATGTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT
CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCCTCTCCCGTAGCCCAACCGA
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCTGGCTACCTCGCCCTGCCTTCAGCCT
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC
CTGCCACCCTCAACGTCCTCAATGGCTCTGACGCCCGCTGCCCTGCACCTTCAACTCCTGC
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCACAACTGCTC
TGAGGAGATGTTCTCCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCCGGTTTCAAG
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTG
CAGCCGGAGGATGAGGGGATTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGG
CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG
CCGTGATTGTGGGTGCCTCCGTGGGGGCTTCTGGCTGTGGTTCATCTGGTGCTGATGGTG
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCGGCC
CTGCAGCCTCCCGTGTCCCGTCTCTCCCTCTCCGCCCTGTACAGTGACCTGCCTGCTCG
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCTCCTGAACCCCG
ACTTCGTATCTCCACCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGCTCCACCTGCCAGTCCCTGG
GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA
GGAGGGGCGCTGTCACTGCCCAGTGCTTGCCTGGCAGTGGCTTACAGAGGAGACCTGGTGG
GGAGGGAGGGCTTTCCTGTGCTGACAGCGCTCCCTCAGGAGGGCTTGGCCTGGCACGGCTG
TGCTCCTCCCTGCTCCAGCCAGAGCAGCCATCAGGCTGGAGTGACGATGAGTTCTCTGA
AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG
CTGCAGGCAAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCAGCGGGACCCACCAACAGAGGCC
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG
GCTCTGCCTTCTCCATGGGGTAACCACCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT
GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCTTGGGGCTTCACTGAGAACTCTCCAGTT
GCCCTTGGTGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCG
GCATAAGGGGAGGCCTTGGAACTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCAGC
CTACTCGCTCCTCTCCCAACAACTCCCTTCGTGGGGACAAAGTGACAAATTGTAGGCCAGGC
ACAGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT
CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAAATTAGCTGGGCGTG
GTGGCGTGCCTGTAAATCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG
GGAAGCAGAGGTTGCAGTGAAGTGAAGTGTAGTGCCTGCAATTACGCTGGGTGAC
ATAGAGAGACTCCATCTCAAAAAA

FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAPSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

FIGURE 56

GTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCCCTCCAG
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACTGCTACATCATGAACCCCC

FIGURE 57

TCACGGGGCTCATCTCTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCCTCAACGTCTCTCAATGGCTTTGACGCCCGCCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAAC TGCTACATCATGAACCCCC

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FIGURE 58

TGCGGCGACCGTTCGTACACCATGGGCGCTCCACCTCGGCCCCCTACCGTGTGGGGCTGCTCCCAGATGGCGCTCCTGT
TCCTCTTGTGTGCTTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGAGCTCACCCCCAGTGGTGTGCTGCTCC
CTGGTGTATTTGGTTAAACCACTGGAAGCCAAAGCTGGACAAGCCGACAGTGGTGCCTACTCTCTGCTCAAGAGA
CCGAAGCTACTTTCACAAATCTGGCTGAACCTGGAACCTGCTGCTGCCTGTATCATTTGACTGCTGGATTGACAATA
TCAGGCTGGTTTACACAAACATCCAGGCGCACCCAGTTTCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG
GGAAGACCTTCTCACTGGAGTTCCTGGACCCAGCAAAAGCAGCGTGGGTTCCTATTTCACACACATGGTGAGA
GCCTTGTGGGCTGGGGCTACACACGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG
AAAACGGGCCCTACTTCTTGGCCCTCGCGAGATGATCGAGGAGATGTACAGCTGTATGGGGGCCCGCTGGTGC
TGGTTGCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGACGCGGAGCCGAGCGCTGGAAGGACAAGT
ATATCCGGGCTTCTGTCTCACTGGGTGGCGCTGGGGGGGCGTGGCCAAAGACCTCGCGCTCTGGCTTCAGGAG
ACAACAACCGGATCCAGTCTATCGGGCCCCGTAAGATCCGGAGCAGCAGCGGTGAGCTGTCTCCACAGCTGGC
TGCTGCCCTACAACACACATGGTCACTGAGAAGTGTTCGTGCAGACACCAACATCAACTACACACTGCGGG
ACTACCGCAAGTTCTTCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGAGGACACAGAAGGGCTGGTGG
AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCTCTATGGTACTGGCGTCCCCACACAGACTCCTTCTACT
ATGAGAGCTTCCTGACCGTGACCCATAAATCTGCTTTGGTGAACGCGATGGTACTGTGAACCTGAAGAGTGCC
TGAGTGCCAGGCTTGGCAGAGCGCCAGGAGCACCAAGTTGTGTCGAGGAGCTGCGAGGACGAGCACATCG
AGATGCTGGCCAAACCCACACCCCTGGCCTATCTGAACAGTGTGCTCCTTGGGCCCCGACTCCTGTGCCACAGGA
CTCCTGTGGCTCGGCCGTGGACCTGCTGTGGCCCTCGGGGCTGTACGGCCACCGCTTTTGCAAAGTTTGTGA
CTCAACATCAAGGCCCGCAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTGTTATCCTTTCTCT
GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAAATGCTGCTGATGGTGA
ACTGCTGTACCTTAGGACTGGCTCCACAGGCTGGACTGGCTGGGCCCCCTGGTCCAGTCCCTGCCCTGGGCGCATG
TGTCCCCCTATTCTGTGGGCTTTTCATACTTGCCCTACTGGGCCCTGGCCCCGAGCCTTCTATGAGGGATGTT
ACTGGGCTGTGGTCTGTACCCAGAGGTCCAGGGGATCGGCTCCTGGCCCCCTGGGTGACCTTCCCAACACCA
GCCACAGATAGGCTGCGCACTGGTCACTGGGTAGCTAGAGCTGTGCGCTTCCCTGTGGCTTAGCTGTGGCCAGCC
TGACTGGCTTCTGGGCGAGCCTAGTAGCTCCTGACAGGCGAGGGCAGTTTGTGCGTTCCTGTGGTTCCAGGC
CCTGGGACATCTCACTCCACTCTACCTCCCTTACCAACAGGAGCATCAAGCTCTGGATTGGGCAGCAGATGTG
CCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGG
CTCCCTTACCCCTGGGACTGTGTTCCAGGATGAGAGCAGGGGTGGAGCCATGGCCTTCTGGGAACCTATGGA
GAAAGGGAATCCAAAGGAAGCAGCAAGGCTGCTGCAGCTTCCCTGAGCTGCACCTCTTGTAACCCACCATCA
CACTCCACCCCTCGCCTAGGCTCTCACTAGTACCAAGTGGTCAAGCAGGCTGAGGATGGGGCTCCTATCCAC
CCTGGCCAGCACCCAGCTTAGTCTGTGGACTAGCCCAAGAACTTGAATGGGACCTGAGAGGCGAGGGGTCCCC
TGAGGCCCCCTAGGGGCTTTCTGTGCGCCAGGCTGCTCCATGATCTCCCTGTGGCAGCAGCATGGAGAT
CAGGGCTGCCCTCATGGCAGTAGGCTCTAAGTGGGTGACTGGCCAGGCGGAGAAAGGGTACAGCCTCTAGGT
GGGGTTCCCAAAGACGCTTCAGGCTGAGCTGAGCTGCTCTCCACAGGCTTTCTGTGACGTGGATTTCCTCTG
TTGCATACATGCTGGCATGTCTCCCTTGTTCCTGAGTGGGCCACATGGGGCTCTGAGCAGGCTGTATCTCTG
GATTCTGGCAATAAAGTACTCTGATGCTGTAAAAAATAAAAAAAAAAAAAA

FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH
YLCSSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGDVVRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNMRI
PVIGPLKIREQQRSVSTSWLLPYNYTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWLM
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLGSP

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACATGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGAAGCAGCCGCA
GGTGGTGGCGCGCGCCGTGTGCTTGCTTCGCGCTTGATCGTGTTCTCCTGCATCTATGGTG
AGGGCTACAGCAATGCCCACAGATCTAAGCAGATGTAAGTCTGCTGTTCAACCGCAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCCTCTCTTGAT
GGTCGACGCGTATTTCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGGTTGGTTCTGCTTCCTCACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCGGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACT
GCCTACGCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGCCTCCCTCTGCCCTGGACTTTCCTCATAGCCTCCTGGAAGTGGCA
GCCCTCTCTTTACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGCTGGCAGAGCCACACCCAAAGTGCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGCACTTTTAGGAAAGGGTTTTAGCTAGTGTTTTCTCGCTTTTAATGA
CCTCAGCCCCGCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCT
CAGCTTCCCCCGGCCCGGTGAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGAGCCGACACAGGCTCTGTGTCTCTCA
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACTGTGCCGGT
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGCTGGTGCTCATGGCACTTCTCCTTG
CTCCACCCCTGCGAGCAGGGAAGGGCTTGCCTGACAACACCCAGCTTTATGTAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGTGCCCCATGGCTCCAGACTCTGTC
TGTGCCGAGTGATTATATAAATCGTGGGGGAGATGCCCGGCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTTCTCATTCAAAG

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVLFALIVFSCIYGE GYSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVI GDLLFSALWTFWLVFGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

FIGURE 62

GAGCCACCTACCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG
 CCCGTGGCCGAGGCCCCCCCAGGTGGCTGGCGGGCAGGGGGACGAGGTTGATGGCGAGGAAGCGGAGCCAGAGGGG
 ATGTTTCAAGGCCCTGTGAGGACTCCAGAGAAAAGCCCGGGGCTACCTCCGCTTGGTGCCCTGTTTGTGCTGCTG
 GCCCTGCTCGTGTGCTGGCTTCGGCGGGGGTGCTACTCTGGTATTCTCAGGTAACAAGGCGAGGTGATGGTCAGC
 CAGGTGTACTCAGGCAGTCTGGCTGTACTCAATCGCCTCTTCCACAGATCTTACCCCGCGGGAACTTAGTGCC
 TTCCGAGTGAAACCGCCAAAGGCCAGAAGATGCTCAAGAGCTCATCACCAGCACCCCGCTCGGGAATCTACTAC
 AACTCAGCTCCGTCTATTCTTTTGGGAGGGACCCCTCACCTGCTTCTTCTGGTTTCTTCCAAATCCCCGAG
 CACCGCCGCTGATGCTGAGGCCCGAGGTTGGTGCAGGCACCTGCTGGTGGAGAGCTGCTGCTCCAGCTCAACAGC
 TCGCTCGCCTCCCTCACGGSCCGAGTACGAAGTGGACCCCGAGGGCTAGTGATCTCTGCGAGGCCAGGTGTGAA
 GACATAGCTGCATTGAATTCACCGCTGGGTTGTTACCGCTACAGCTACGTTGGCCAGGGCCAGGTCTCCGGCTG
 AAGGGCCCTGACCACTTGGCTCCAGCTGCTGTGGCACTCGAGGGCCCCCAAGGACCTCATGCTCAAACTCCGG
 CTGGAGTGGAGCGCTGGCAGAGTGCCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCTGGAGAAAGAGGCTC
 ATCACTCGGTGTACGGCTGCAGCGCCAGGAGCCCGTGGTGGAGGTTCTGGCTCGGGGGCCATCATGGCGGTG
 GTCTGGAAGAAGGGCCTGCAAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCGTG
 GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCAGGGCGTCTCAGCACCCCGTACTTCCCGAGCTACTAC
 TCGCCCCAAACCACTGCTCCTGGCACTCAGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGTATGCC
 TATGCACTGAGGAGGCAGAAATGATGATTTGCCGTGCACCCAGGGCCAGTGGACGATCCAGAAACAGGAGGCTGTG
 GGCTTGGCATCCTGCAAGCCCTACGCGAGAGGATCCCGGTGGTGGCCAGGCCGGGATCACCATCAACTTCACC
 TCCAGATCTCCCTCACCGGGCCCGGTGTGGGGTGCACTATGGCTGTACAACAGCTCGGACCCCTGCGCTTGA
 GAGTTCTCTGTCTGTGAATGGAATCTGTGCTCCTGCTGTGATGGGGTCAAGGATGCCCCAACGGCCCTGGAT
 GAGAGAACTCGCTTTGCAAGGCCACATTCAGTGCAAAAGAGGACAGCACATGCATCTCACTGCCCAAGGTCTGT
 GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACC
 TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGGCCGACTGCAAGGACCGC
 TCGGATGAGGAGCACTGTGACTGTGGCTCCAGGGCCCTCCAGCCGCAITGTTGGTGGAGCTGTGCTCTCCGAG
 GGTGATGGCCATGGCAGGCCAGCTCCAGGTTCCGGGTGCAACATCTGTGGGGGGGCCCTCATCGCTGACCCG
 TGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCCTCCAGGGTGTGTGGACCGTGTCTCTGGGC
 AAGGTGTGGCAGAACTCGCGCTGGCTGGAGAGGTGTCTTCAAGGTGAGCGCCCTGCTCTGTCACCCGCTACAC
 GAAGAGGACAGCCATGACTACGAGCTGGCGCTGTGCGACTCGACACCCTGCTGGCGCTCGGCGCCGCTGCGC
 CCGCTCTGCTGCCCGCGCTCCCACTTCTTCGAGCCCGGCTGCACTGCTGGATTACGGGCTGGGGCGCCTTG
 CGCGAGGGCGGGCCCATCAGCAAAGCTCTCGAGAAAGTGGATGTGCAGTTGATGCCACAGAGACCTGTGCAGCGAG
 GCTATCGCTACAGGCTGACGCAAGCATGCTGTGTGCGGGCTACCGCAAGGGCAAGAAAGATGCTGTCAAGGT
 GACTCAGGTGGTTCGCTGGTGTGCAAGGCACTCAGTGGCGCTGGTTCCGGCGGGCTGGTCAAGTGGGGCTG
 GGCTGTGGCCGGCTCAACTACTTCGGCGTCTACCCGCTACACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
 AACTGAGGAAGTCCGCCCTGCAAGAGCGGCCCTCCTCTCTGACTCAGAGAGCCAGGGCACTGCCAGCAGG
 GGCACAGTATTCTTGGCGGGGGGTGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGTGGCATCTTCTGTGCTGCC
 CTGATGTCTGCTCCAGTGTATGGCAGGAGGATGGAGAGTGCCAGCAGCTGGGGGTCAAGAGCTGCCCTGAGGACC
 CAGGCCACACCCAGCCCTTCTGCTCCCAATCTCTCTCTCCGTCCCTTCTCTCCACTGTCGCTAATGCAAG
 GCAGTGGCTCAGCAGCAAGAAATGCTGGTTCTACATCCGAGGAGTGTCTGAGGTGCGGCCCATCTGTATCAGAGG
 CTGTTTGGGCGCCCTTGGCTCCAGAGAGCAGATTCAGCTTCGGAAGCCCTGGTCTAACTTGGGATCTGGGAAT
 GGAAGGTGCTCCCATCGGAGGGGACCTCAGAGCCCTGGAGACTGCCAGGTGGGCTGCTGCCATGTGAAGCAA
 AAGGTGGGAGTCTCTGACTCCAGGGTCTTGGCCCAACCTGCTGCCATGCTGGGCCCTCAGGCCACGACCTT
 CACTGGGAGGTGAGCTCAGCTGCCCTTTGGATAAAGCTGCTGTATCAAAAAAAAAAAAAAAAAAAAA

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGQGDDGEEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSVQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRIGT
YNNSSSVSYFGEGLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLKGPDLASSCLLWHLQGPDKDML
KLRLLEWTLAECRDLRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPFVVFQACEVNLTLDNRLDSQGVLSSTPYFPSPYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPCTQGQWTIONRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPEGLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKPNPQCDGRPCDRDGSDEEHCD
CGLQGPSSRIVGGAVSSEGEWFWQASLQVRGRHICGGALIAADRVITAACHCFQEDSMASVTL
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDGSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQVVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC
CTGGAGAGTTCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGA
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGATTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTCGGGGTCGACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGACAGCAT
GGCCTCCACGGTGCTGTGGACCGTGTTCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCAGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGTGTCAGCTCGACCAACCCGGTGGTGCCTCGGCCGCCGTGCGCCC
CGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGTGACTCAGTGGTCCGCTGGTGTGCA
AGGCATCTAGTGGCCGCTGGTTCCTGGCGGGCTGGTCACTGGGGCTGGGCTGTGGCCGG
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

[illegible]

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVFPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHLKLVSAHHTREKDANVVVDWL
PLAHQLYTDVANNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGCLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKMRNRKRNKMYLKTRAGMPFRGNLQSLQEC

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

FIGURE 67

CGGACGCGTGGCGGAGCGTGGGCGCTGGGCAAGGCGGGGGCGCGGGCGAGGCCACCTCTTCCCCTCCCCGCG
 TTCCCTGTGCGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGCGCGGCTTGGGGGCTGACAGT
 CGGCAAAATTTTGGCCCGAAGAGGAAGTGGTCTCAAACCCCGGACAGGTGGCGACGAGCGCAGACCAAGGGGCGCTCG
 CTGCTCGCGGGCGGCTGTAGGCGAGGGCGCGCCCAAGTGCAGAGCCAGCGGGCTTCAGGAGCGCGGCCCGGGAG
 AGAAGAGTTCGCGCGGGACGAGAGAAACAACTCCAAGTTGGCGAAAGGCACCGCCCTACTCCCGGGCTCGCG
 CCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGAGAGCCCCCTGGGAGGCGG
 CACCAAGGAGGCTGGGGCGCCCGGGGCTCCGCGCGACCCCATCGGTAGACCAAGAAGCTCGGGAACCTTCCCG
 GCACCTCTGGAGCAGCCAGGATGCTGTGGCCACCCCTCTCCTCTCTCTTGGAGGGCGCTCTGGGCCATCCAG
 ACCGGATTATTTTCCAATCATGCTGTGAGGACCCCCAGCAGTGTCTTTAGAAGTGCAGGCGCACTTACAGA
 GGCCCCGTGGTTCGGGACAGCGCACCTCCCTGCCAACTGCACCTGGCTCATCTCGGCGAGCAAGGAACAGACTG
 TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCTTAGCCTCCCTCTCCAGGCCAC
 TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCGGGGGCAACGTCAACATCACTTACAGCTATG
 CTGGGCGCAGAGCACCATGGGCCAGGGCTTCTGCTCTCTACAGCCAAAGATTGGCTGATGTGCTGCAAGGAAG
 AGTTTTAGTGCCGTAACACCCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGTGTGATGCGCTGTGGCGATGGCT
 CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCTCTGGCTGACCCCAAGACCGCTCCCTCTCTGCTGTGCAATG
 TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCTCTGGATATACACACCTTAGCCTCAGTCTCCACCCCCAGT
 CCTGCCATTGGCTGTGGACCCCCATGATGGCCGGCGGCTGGCCGTGCGCTTCACAGCCCTGGACTTGGGCTTTG
 GAGATGCAGTGATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCTAGTCTCACCCACTTCA
 GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTTACACACAGTGTGCTGGAGCA
 ATGGTGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCCTGGGACAGACCCCTGTGGCTTAGGCT
 CTGGCTTGGGAGCTGGCGAAGGCTTAGGTGAGCGCTGTACAGTGAGGACAGCGCTGTGACGGCTCATGGGACT
 GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTCTGTGGGCTGCTGGCACCT
 CTGGTGCCACAGCTGTCTAGTGCCTGTGACCGCTGCACTACACAGACTTCTGTGCTGATGGAGCAGATGAGA
 GACGCTGTGGGCTTGGCAGCTTGGCAATTTCCGATGCCGGGAGAGAGTGGCTGTATGAGAGCTGGGTGTGCG
 ATGGGACGCGCAGTGTGCGGACGGCAGTGTGATGAGTGGGACTGTCTCTATGTTTGGCCCCGAAAGGCTCATACAG
 CTGAGCATCTTGGCAGCTAGTGTGCGCCGTGCTCTGGTCTATGGCCCTGGGCTGCAAGCTCTATGCCA
 TTCCGACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGACCCCC
 TCTCTCAAGGAGTCTATGTGCCAGGGTGCATCCCACTGTAGAGACTTCTCTCAAGAGAACTCAATATGATA
 ACTCAGTGTGGGCAACCTCGGTCTCTGTCTACAGATCTTAGCCAGGATGACTCCAGAGGTTGGCCCGAGTG
 CCCCCTGTCTGAGCGGGGCGCTGTATGCGACGCTGGTACGCCCTCTCCGCGCTGTGGGGCTTGCTCTCGAA
 CCAACACCCGCTCGGGCTCTGAGGCGCAGATCCAGTCAACCTTCTGTGCTCCCTTGGAGCCCTTAGATG
 GTGGCACAGTCTCAGCCCGTGAAGGCGGGCAGTGGGTGGCAAGATGGGGAGAGGCACCCCACTGCCCATCA
 AGGCTCCCCCTCCATCTGCTAGCAGCTCTCCAGCCCCACTATGTCTCTGAGCCCCAGGSCCATGCGCTCAC
 TGCCCCCTAGAGCCATCACTATTGCTGAGTGGTGCAGGCCCTGCGAGCGCGCTGTGCCACCTGGGGCCCC
 CTCTACTGAGGCTCTCCCTTGGGGGCTTACTCATAGTGGCAACACCTTTTAGAGGTGGGTGAGCTCTCCCTCC
 ACCACTTCTCTCCCTGTCCCTGGATTTCAGGGACTTGGTGGGCTCCCGTTGACCCCTATGTAGCTGTCTATAAAGT
 TAAAGTTCCTCAGGCGAGGAGAGGGCTCACAGAGTCTCCTGTGTAGCTGGCCAGCCAGACACCCCACTCCCT
 TCACCAACCACTGCTCCCCAGCCACCACTTTGGGTGGCTGTTTTAAAAAGTAAAGTTCTTAGAGGATCAT
 GGTCTGACACTTCATCTTGGCAAACTCTACCCAAAAGTGGCTTAAGCACCGGAATGCCAATTAACATAGAGA
 CCCCCTCAGCCCCAAGGGAGGATTGGGCAAGAACCTGAGGTTTTCATCCACAACTCCCTCTCAGGGCGCTGG
 CTCACAAAAGAGTCAACAAATGCTTCTATTCCATAGCTAGCGCATTGCTCAGTAAGTTGAGGTCAAAATAA
 GGAATCATACATCTC

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHPDRIIFPNHACEDPPAVLLEVQGTQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSLPLQLPLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEETFQCLNHRCSVSAVQRCDGVDACDGSDEAGCSSDPFPGLTPRP
VPSLPCNVLTLEDIFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRRLAVRFTALDLGFGDAVH
VYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP
WDRPCGLGSLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPGHPFCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRCRDEKCVYETWVCDGQPD CADGSDEWDCS
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIPPVEDFPPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGLMRRLVR
RLRRWGLLPRNTNTPARASEARSQVTPSAAPLEALDGGTGTPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLPSLPGPPGPTRSPPGPHTAV
LALEDEDDVLLVPLAEPGVVVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTGCTATCGCTTCG
CAGAACCCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCTGAACCATATATTGTTATCACTGGATTGGAAGTCACCGTTATCTTATTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAGAAGTTTGTAATTTTTATATTACTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

1000
900
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700
600
500
400
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100
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FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPFPYIVITGFEVTVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVAVCCCLAD
GALIYRKLLFNPSGFPYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCGCGCGGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCCTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

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FIGURE 72

CAGCCCCGCGCGCCGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCGCGCGTGGGCATGGGCGCACTGGCCCCGGCGCTGCTGCTGC
CTCTGCTGGCCAGTGGCTCCTGCGCGCCGCCGAGCTGGCCCCCGGCCCTTTCAGCGTG
CCCCTCGGGTGGCCGCGGCCACGAACCGGTAGTTGCGCCCCACCCCGGACCCGGGACCCC
TGCCGAGCGCCACGCCGACGGCTTGCGCTCGCCCTGGAGCCTGCCTGGCGTCCCCCGCGG
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAGGCTTCAACTACTTCTTTTCTTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCCTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAAGGAAGAGTGGTACTACCAGATAGAAAATCTG
AAATTGGAATTTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCTGGACAGTGGCACCACGCTGCTGCGCCTGCCCAGAAGGTGTTTGATGCGGTGGTGG
AAGCTGTGCCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG
CTGGCGTGCTGGACGAATTGCGAAACACCTTGGTCTTACTTCCCTAAAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCATTCGGTATCACAATCCTGCCTCAGCTTTACATTTCAGC
CCATGATGGGGGCCGGCTGAATTATGAATGTTACCGATTGCGCATTTCCCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA
GAGGGTGGGCTTCGACGCGAGCCCCGTGTCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCTTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCCTT
AATCGTCCTGCTGCTGCTGCCGTTCGGGTGTGAGCGTCGCCCCCGTGACCTGAGGTGCTCA
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACCTCAGCTATTAAGAAAATCACATTTCCAGGCGAGCAGCCGGGATCGATGGTGGCG
CTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTAC
TGTCCTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTA
AAAAAAACTTCATTCTAA

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPPTPAERHADGLAL
ALEPALASPAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYDTERSSTYRSKGFDTVVKYTQGSWTGFGEDLVTIPKGFNTSFLVNIATIFESENF
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFASPCA
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCGAILLVLLVLLLLPFR
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

FIGURE 74

CGCCTCCGCCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGCGCATCCAGGGCGGTGCGGGCCCTGGCGGGAGCCGGGAGCGCGGCC
GGCATGGAGGCGCTGCTGCTGGGCGCGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCCGACGGCCCGTGG
TCACGGGCGCCAAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGTGCTGGCCTGCCGAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGAGACCCGTGAGGCGTTTAACTGCTGCTTTCGGGTGAACCATAT
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCCCTGAAGGCATGTGCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCCACTGTGCGGGACGTCTTGACTTCAAACGCTTGGACCGC
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGAGCTCGCCAAACAGCTTGAGGCCACTTGGCGTCACTGCTATGCAGCCACC
CAGGGCCTGTGAACTCGGAGCTGTTCTCGGCCATGTTCTCGGATGGCTGCGCCCACTTTTG
CGCCCATTTGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGTGCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTGCCAACTGCCATGTGGAAG
AGGTGCCTCCAGCTGCCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCACTGTGAGGACTC
AGAGGCCCATCTTCTCTAAGCACCCCCACCCCTGAGGAGCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCTTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGTCCTT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTCTGTTGAAGGAAT
AATGGGTGATTATTTCTCTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTTGATGTAGTATTTTCAGGCCCCACCTTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
TGAAGTATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGCCTG
GGATCTGAACCCAAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG
ATGCAGGGCTGGGGTCTATCTGTATCTGAAGCCCTCGGAATAAGCGCGTTGACCGCCAAA
AAAAAAAAAAAAAAAA

FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGTAVVTGANSIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRLD FKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCTYAAHPGFPVNSELFLRHVPGWLRPLL
PLAWLVLRAPRGAQTPLYCALQEGIEPLSGRYFANCHVEEVPAAARDDRAAHLWEASKRL
AGLGPGEDAEFDEDPQSEDSEAPSSSLSTPHPEEPTVSQPYSPQSSPDLSKMTMRIQAKVEP
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

FIGURE 76

GGAGGAGACAGCCCTCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGAGGCGATGGCTCAG
GACTCCCGCCCCAGATCTCTAGTCCACCCACAGGACAGCTGTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC
CAGGCTCTCAGGCGAGCCACTCCCCACCATCCGCTGCTGTCTGAATGGGCGAGCCCTGAGCATGGTGGCCAGGAC
CCAACACACCTCTGCTGCTGATGGGACCCCTTCTGCTGCTA.CAGCCCCCTGCCCGGGGACATGCCACAGATGGCCAG
GCCCTGTCCACAGACCTGGGTTGTACACATGTGAGGCGCAGCAACCGGCTTGCCACGCGAGCTCAGCAGAGGCGCT
CGGCTGTCTGTGGCTGTCTCCGGGAGGATTCAGATCCAGCTCCGGGACATGGTGGCTGTGGTGGGTGAGCAG
TTTACTCTGGAATGTGGGCGGCCCTGGGGCCACCCAGAGCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG
GCCCTCAGGCCCGGAAGGACACAGTGTCCGGGGGCTCCTGCTGATGGCAAGGACAGAGAAGTGTACGAGAGG
ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGAGAGCGCGCAGCCGGGTTTCATCCAGGAGGCC
CAGGACTACAGGAGCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAATGTGACACTCCTGCAACCCGAGT
CCTGCAGAGGGCCCCAAGCCTAGACCGCGGCTGTGGCTCAGCTGGAAGGTCAGTGGCCCTGCTGCGCTGTGCCAA
TCTTACACGGCTTGTTCAGGACCCAGACTGCCCGGGAGGCCAGGGAGCTCCGTGGGCGAGAGGAGCTGTGGCC
GGCTGGCAGAGCGCAGAGCTTGGAGGCTCCTACTGGGCGCAAGACTACAGATTCAAAGTGAACCATCTCTGGC
CGGCTCGAGGCCCTGACAGCAACGCTGCTGCTCCTGAGGCTGCCGGAATAAGTCCAGTGCACCTCAGGAA
GTGACTCTAAAGCTGGCAATGGCACTGTCTTTGTAGAGCTGGGTCCCAACACCTGCTGAAACCACAATGGCATC
ATCCGTGGCTACAGGCTGTGAGGCTGGGCAACACATCATCTGCCACAGCCAACTGGACTGTAGTTGGTGAGCAG
ACCCAGCTGGAAATGCCCAACCATATGCCAGGCTCCTACTGCTGCAAGTGGCTGCAGTCACTGGTGTCTGGAGCT
GGGGAGCCCATAGACTGCTCTGCTCCTCTTTAGAGCAGGCGTGGAGCGAGCCCAAGAACCCAGTGAAGCT
GGTCCCTGGACCTTGGAGAGCTGAGGGCTACCTTGAAGCGGCTGAGGTCAITGGCACTGCGGTGTGTGCACTC
TGCTGTGCTTCTGGGCAACCGCGCTGTGTATCCACCGCGGCGCGAGCTGAGGTGCACTGGGGTGCACTGGGCTG
TACAGATATACAGTGAAGTGCATCCTATAAAACACAGGATGGATCAAGTGACTCCAGTGGTGGCAGACACT
TGGCGTTCCACTCTGGGCTCTGGGACCTGAGCAGCAGCAGGCTCAGCAGTGGCTGGGGCGGATGCCCGG
GACCCACTAGACTGTGCTGCTCTGCTCTCCTGGGACTCCCGAAGCCCGCGGTGCCCTGCTTCAGACACC
AGCACTTTTATGCTCCTCATCTGCTGAGCTGCCCTCCAGTACCCAGCCAGGCAAGTCCCGAGTCCAGCT
GTGAGGCGCTCCCAACCCAGCTGGCCAGCTCTCCAGCCCTGTTCAGCTCAGACGCTCTGAGCCGCGAGG
GGACTCTTCTTCCCGCTTGTCTTGGCCCTGCTGAGAGCTTGGAGGCCCAAAAGAGCAGGAGCTCAGCAT
GCCACAGTTTCCCACTGCTCCGGGCGAGCACTCCTTGGAGCTCCGGCTCTGTAGTTAGGAATATAGAGTTCC
AAGAACCTTTCCCAAAGCCAGGAGCTGTGCCCAAGCTCTGTTGCTGCCCGGGCTGGGACCGAAACTCCTC
AGCTCCTCAAATGAGCTGGTATCTCTCTCATCTCCCTCCAGCACCCCTCTTCTCATGAACTCCCCACTCAG
AGTCAACAGAGCCCGCTCCGTTGGCACCACAGGCTCCCTCCTCACTCTGCTGCCAGCAGCCCACTCCCATC
CTTAGCCCTCGAGTCCCTTAGCCCCCAGGGCTCTTCCCTCTCTGSCCCACGCCAGCTTCCAGTCCGCTGTCC
AGCTCCTCATCTGTATCCTCTGGGGGAGGATCAAGACAGCGTGTGCTGACCCCTGAGGAGGTGTCTGGAA
CTCAGTGAGGGTGAGGAGACTCCAGGAACAGCGTCTCTCCATGCCAGCAGGCTCCCTTCCACCCCAACCACTAT
GGGTACATCAGCGTCCCAACAGCTCAGAGTTCAAGGACATGGGCGAGGACTGAGGAGGGCTGGGGCCAGGGG
GGAGTCTTGTGTGCCCACTCGGCCCTGCTTCACCCCACCCCCCAGGAGGCTCTTAGCCCAATGGTTGGGGC
TCAGCCTCTGAGGACAATCGCGCAGCGCAGAGCCAGCCTTGTGAGCTCTCCGATGGCTCTTCTCTCGTGTAT
GCTCACTTTGCCCGGGCTCGCAGTGGCTGTGGATAGCTTTGGTTCTGAGTCTGAGGCCAGGGAGGCGAGCTGC
GTCTTCATAGATGCTCATCATCTCCCTCCCAACCGGATGAGATCTTCTGAGCCCAACCTCTCTCTGCCCTC
TGGAGGTGGAGGCGAGCTGGTTTGAAGACATGGAGGTTCAGCACACCCAGCGGTGGGAAGGGGGATGCCTCC
TGGCCCCCTGACTCTCAGATCTCTTCCAGAGAAGTCACTCCTGTCGTATGCCAAGGCTGGTGTCTCTCTCT
GTAGATTCTCTCTGAAGAGCTGCTGAGACTTCCAGACGGGAATCAGAACCACTTCTCTGTCCACCCAAAG
ACCTGGGGCTGTGGTGTGGGCTCTTGGCCTGTGTTCTCTGCACTGGGGTCACTCTCCCAAGCCTCAGAGAG
TTCTCCTCCAGATTGTGAAACAAATGAAACAAATATGAGACCAAGCTCCTGAGGCCCTCAGGAGCCCAAA
ACATCATCTCCACTGACTCTAGCCACTGCTTCTCTCTGTGCCATCCACTCCCAACACAGAGTTGTTTGCTT
CTGAGGAGCAGCGCTGCTGTGCTCTTCCCACTTTGGATCACAGGAAGTGGAGGAGCCAGAGGTGGGCTGT
GTGGAGGACAGCAGTGGCTGTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGAGCCCCCTCTCAGCCTTACT
GGCGCCCTCTCTAGAGAGGACTCAACTCTCTCCAACTCACCATGGAAAGAAATAATATGAATGCCACTG
AGGCATGAGGCCCTACTCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGTCTAGAGGAAGGGAG
TATGAGACGTTAGGTCAAAGACCACTCTCGTACTGTGTGTCTACTAGCTTAAGAAATTTGATACCTATAAAT
GGTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSFPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDDEGTYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPDPAEGPKRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSABELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPAENHNGIIRGYQVWSLGNSTLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEFSRPVCLLEQAMERATQEPSEHGFW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTS
FYGSLIAELPSSPTAPRSPQVPAVRRLFPQLAQLSSPCSSSDSLCSRRLSSPRLSLAPAEA
WKAKKKQELQHANS SPLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAVRALGPKLLS
SSNELVTRHLPAPLFPHETPPTQSQQTPPVAPQAPSSILLPAAPILSPCSPSPQASS
LSGSPASSRLSSSSLSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWGSASEDNAAASARA
SLVSSSDGSFLADAHFARALAVADSFGFGLPEPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHTQRLGRGMFPWPPDSQISSQRSQLHCRMPKAGASPVVDS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGAGGAGGGGT
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCTTGTGGA
 ACCTCACCTTGCAGAGCCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCGATGAG
 TCTTTACTACTCTCTGTTCGTCTTTCCAGGACCTGTGTCTCCTCCCTCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCCAAAGCTCAGCAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCAATGACAG
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTTAAGCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTCTGCTGAGCCTTCTGTACGC
 CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCTTGACTTCGGAGGAAAGGAAGCC
 CCTTCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGGATTCCCGAAAGCTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCAGGAGCTCTCCCAACCTCCCAAGGCTCTCCTCTTGATGTTTCA
 GCCTGACCTAGAAGCGTTTGTGAGCCTGGAGCCAGAGCGGTGGCCTTGTCTCTCCGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC
 CTCATGCCCCAGTGTGCGACCCCTGCCTTCTCCCACTCCGAGCCCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCAACGGTCTCCTGCATCAGCTGGTGTGTAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTTCAGGAAGCCT
 GTGAAAAACGTGATTCTCGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTAAACCAATGCCAGTGAAGTGTGCACTTGAAGTTTGAAGGCCAGTGGGCCGT
 ATGAACGCTCACCAACCTTTCAGCTTAGAGTCTGCATTGGGCTGTGACGTCTCCACTGCCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGAACCTCCCTGAGGCCCTGCTAAG
 TCCAGGCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCCTTTNCCATTTGCCCCCTCCCTGGNCCATGCCTTCTTGCCCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTGTCTGGAAGGGGTTACTTGCCTATGGGTCTGTGTGGCTAGAGA
 GAAAGTAGAAAAACAGAGTGCACGTAGTGTCTAACACAGAGGAGATAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCAGTCCAGTCCAGCCCGCTGGAGAAGGGGTGGGGGTGGTGGTAAAGTA
 GCACCACTACTATTTTTTTCTTTTCCATTATTTGTTTTTAAAGACAGAATCTCGTGTCT
 GCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCCGCTCCTGGGTCAAGTGATT
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCCACCACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCCTGCTCAGTCTCCAAATTCGCCGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCTTTTAAAAAGTGAATTAAGAGTTGTTTCAATGATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAGAAAGAAAAAATGTCAACCTAGTCTCACCAGAGACTATCAT
 TATTTCTGTTTTGTGTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT
 TTTACAGAGCAATTTATCTGTATATACAACCTTTGTATCCTGCCCTTTCCACCTTATCGTTCC
 ATCACTTTATTCAGCACTTCTCTGTGTTTACAGACCTTTTATAAATAAATGTTATCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSI RDSRQELSLIVTLWNLTLDAGEYWC GVEKRGPDESLLISLFV
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGA EAPPLPG
TSQYGHERTSQYTGTSHPHPATSP PAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCA CGGAGGCTGGTGAGCTGCCTGT CATCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGA ACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATAACGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTCA CAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCACAA
ACGGGATCTTCCAGATCAACAGCCGAGGTGGTGAGCAACCTCACCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGTTCTTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCNSLTPNVFNVCRMVCSDLLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGCF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCGCGGCGGCACCATGAGTCCCCGCTCGTGCTGCGTTTC
GCTGCGCCTCCTCGTCTTCGCGCTCTTCTCAGCCGCGCGAGCAACTGGCTGTACCTGGCCA
AGCTGTCTGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCGCGCTGCG
CCAGCTGGCCATTGAGGAGTGCAGTACCAGTTCCGGAACCGGCGCTGGAACGTCTCCACAC
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGCGTGAGCAGTGGGGAGCT
GGAGAAGTGGGCTGTGACAGGACAGTGCATGGGGTACGCCACAGGGCTTCAGTGGTCAG
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCAGTCGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGCTCTGTCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG
GAAGGCCATCTGACACACATGCGGTGGAATGCAAGTGCCACGGGGTGTGAGGCTCTGTG
AGGTAAGACGTGCTGGCGAGCCGTGCGCCCTTCCGCCAGTGGGTACGCACTGAAGGAG
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGTCTCTCAGGGCACTGGTACC
ACGCAACGCACAGTTCAGGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGCGTGTCTGGGCACGAGGGGCCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAAACGTGACAGTGCAAATTCACCTGGTGTCTGCTTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACGCCGCTGCCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCAGGGAAGGCCGATAAATTTAAACAGTCTCCACCACCTACCCCAAGA
GATACTGGTTGTATTTTTTGTCTGTTTGGTTTTTGGTCTCTCATGTTATTTATTGCCGAA
ACCAGGCAGGCAACCCCAAGGCCACCAACAGGGCCTCCCCAAAGCTGGGCCTTTGTGGCT
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCCATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGACAGACCTAAGGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTCTATCGGGGAAGAGGGGCCCTTATGGCAGGGAATA
GGTACCGACTTGATGGAAGTCACACCTCTGAAAAAAGAACTCTTAACCTCTCCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
GAACAAGCAGATACAGGTCAAGGGCACCAGGTTCAATTCAGCCCTTACATGACAGCTAGA
GGTTCGATATCTGTGGGTCTTCCAGGCAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
GTCCCAACCTAGAAACCCAGCCTGCCCCAGCCTGCCCTGGGAAGAGGAACTTAAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACAGGGATCCCGGCTGTGCCTT
TGCAGTCATGCCCGAGTCACCTTTCACAGCGCTGTTCTCTCATGAAACTGAAAAACACACAC
ACACACACACACACACACACACACACACACACAGGACACACACACACACCTGCGAGA
GAGAGGGAGGAAGGGCTGTGCCCTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCTCT

FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEETCEKLKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRWNCSTLDSLFPVFGKVVTQGTREAAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM
NLHNNEAGRKAILLTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCACAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGTCCCCGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC
ACCACAGTCCITTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG
GTGCCCTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCCTGAGG
GCTGTGCGCCATCTGGGGCAAGTTCAAGGCTACCAAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACAGGGAGAGCCCCAATGACGCTTGGGGGCGCGAGAACCTGTGTCTATGATGC
TGCAACGCGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGCGCTGGATCTGTGAG
AAAAGGCACAACCTGCTTGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTCGAGCATGTCGTA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCTAACTCCACTCACGCAGACCAACCTAACC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACTGGA
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSSEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCSGTQAQLQTTRAELGEAQAKLMEQESALR
ELRERVTTQGLAEAGRGREDVRTELFRALAEAVRLQNNSCPECPPTSWSLSEFGSCYFFSVPKTTW
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCGCCCCCGCAGCCCCCTTCTCTCCTTTCTCCACGTCTATCTGCCTCTCG
CTGGAGGCGAGCCGTGCAGCATCGAAGACAGGAGGAACCTGGAGCCTCATTGGCCGGCCCCG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
CGCGCTCCCCTGCTCCTGCGCGGTGATGAAAAACCCAGCCCGGCCCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCGGCCAGCCTCTGGGGGAGAGTC
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
CGGCCTTCCCAAGCAGTACCCCCGTTCGCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTACGTAACGGGCTGCG
CGACTTTCGCGAGCGCGGCGAGGCTGGGCGCTGATGAAGGAGATCGAGGCGCGGGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCGTCCCAGCGGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACCTCGCTGGTCTCGTTTGTGTGCGCATCGTGCC
CAGCCCCGACTGGTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCTACGACGCGGGACGGACAGCGGCTTCACCTTCTCC
TCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCCAG
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAGAAACGCCGCTGGAATGCGAGGTCTC
CCTGTGGTGTCTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGTACGTCCGGGTCCAGCCCCCAACAACGGGAGCCCCGCCCCGAGCTCGAAGAAGAG
GCTGAGTGCCTCCCTGATAACTGCGTCTTAAGACCAGAGCCCCGACGCCCTGGGGCCCCCG
GAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCGGAGGGCACAGGG
GGTTTTGCGCTGCTCTGACCGCGGTGAGGCCGCGCCGACCATTCTGCACTGAAGGGCCCT
CTGGTGGCGGCGACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCGTGTCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCAGGAGATTGTCTTCATCG
TCCAGGGGCTGGCTCCACGTGGTTGCAGATACCTCAGACCTGGTGTCTTAGGCTGTGCTG
AGCCCACTCTCCGAGGGCGCATCCAAGCGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAHSSDYSMWKRNQYVVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSDLCDGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPAPVLPSPDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTRYVRVQPA
NNGSPCPELEEEAECPDNCV

Important features:

Signal peptide:

amino acids 1-26

FIGURE 88

GGCGCGCTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGCTCTTGCGTGA
TATTGACAACTGAAGCTTTCTCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA
CAGCTTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATTGAAAATA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGACAGAAATTTT
ATCCAACCTTTGTTTGGAAAGCTTATTATGACAATACCATTTTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTTCATTACGGTTGCGTTTTAATCGGAGAGGAGTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTCGAGCAGATGAAC
TAACAATAAGCATACCATTCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGCCACATAATCCACACAAAATAAAAGCTGT
GAGGTTTTGTTTAACTCCTTTTGATGACATCATTCGAAGGAAATTAAAGGCTGAAAAAGA
GAAACGAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTCCAGT
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAA
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAACGGGAACCTTTAGCAG
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAAGCAGAAAAAAGAAGTGAAGAGGAAGAA
GCCCCCTCCAGATGGTGTGTTGCGGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACTTCCCGGAAGATCAGACCCCTGCACTGTGTAACCACT
TTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAAGAAGGAGGGAAGAAAAGCAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAAT
GAGAATAATGATAACCAAGAACTTGCTGGAATGTGCCTACATGCGCTTGTAAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACTGTGCTGTGTTTTG
AAAAACAATTATCTTGTTTTGCAATTTGTGAATGATGTAAGCAATGCTTTTGGTTACTGG
TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT
TCCACAAAAA

FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTNGKVLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLEVDIDDDERPHNPHKIKSCEVLFPFPDDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEEAEEEEEEVNVRVQSMKGKSKSSHLLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERI AKKLK KDT SANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAAPPDGAVAEYRREKQKYEALRK
QQSKKGT SREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWM SHVLQFEDKSRKVK
DASMQDSDTFEIYDPRNPVNKRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

FIGURE 90

CGCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCTGCGGGCGAGAGAGATGCTGCCCGG
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTCGCGCTTGCTGACGGCGTGC
AGCCCTGGCCAGACATGTTCCACAGGGTTCCTCTCGGGTCCGGGACTCTGGGCTCCACCCACC
GTGGCCGCGCGGGACAGCACAGGCGGGCTTTCTCCTTCGGAACGGGAACGTCTAGCAA
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG
CTCCTTCAAGTGGTTTGGAAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
GGAGGAACAAATACAGGTGCCTTGACACCAAGAGGCCCTCAAGTGGTCAACAAATATGGAAC
CTGCAAGGAAAAAGATGCATGTGGGGAAAGACCCCATCCAAGTCTTTTAGGAGTCCCCT
TCTCCAGACCTCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGAGGCCCTGGAAA
GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCGCAGGCTGGAG
TGCAGTGGCAGCATCTCGGCTCACTGCAACCTCCGCCCTCCCGGGTCAAGCGAGTCTCCTGC
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTTGGGGCCAGCTGGCCTCG
ATGTACGTCAAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
GAACGTGTACGCGCGCGCGCGCGCGCGGGGATCCCGAGCTGCCAGTGTATGTTCTGGTTCC
CGGGAGGCGCCTTATCTGTTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCGCGC
GAGAAAGTGGTGTGTTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA
CGACAGCCAGCGCGCGGGAACCTGGGGGCTGCTGGACAGATGGCGGCTCTGCGCTGGGTGC
AGGAGAAATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCCTGTTCCGGCCAGTCCGGCG
GGGGCCATGAGCATCTCAGGACTGATGATGTCAACCCCTAGCCTCGGGTCTCTTCCATCGGGC
CATTTCCAGAGTGGCACCGCGTTATTACAGACTTTTCATCACTAGTAACCCACTGAAAGTGG
CCAAGAAGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTCCAAC
TGAACCTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
TGATCCAGATGACCCCTTTGGTGTCTCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCCTTATAATATCACCAGGAGCAGGT
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACATGCAGACTGCTCAC
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGTGGCCACGCTACAACAAGGATGAA
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGGAAGCTCAAGGAGAAGAAGATGGC
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
TGGAATACCTCGGGGACAAGAGTTCTACCCACCCAGTTTAGAATGCAAGGAGCTCCTGTCT
GCCTCAGGCCAAAGCTAGAGCTTTTGCTGTGTTGTGGGACCTGCATCGCCCTTTCCAGCC
TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
ACCACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTCCCTTCTTCAAATCTCT
CCCACCTTCAATGTCTCCTGTGACTCCTTCTTATGGGAGGTGCACCCAGACTGCCACTGC
CCCTGTCACTGCACCCAGCTTGGCATTTACCATCCATCCTGCTCAACCTTGTCTCTGTCTGT
TCACATTGGCTCAGGCGCTAGGGCAGGTTGTGACATGGAGCAAACTTTTGGTAGTTTGGGA
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAGTCTATACACAGGGGTGG
TCTCTTCAATAAAGAGTGTGTATAGAAAAA

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSG
FGTGLFGSKPATGFTLGSTNTGALHTKRPQVVTKYGTLQ GKQMHVGKTP IQVFLGVPF SRPP
LGILRFAPPEPPEPWKGIRDATTYPGWQLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHR LGIFGFLSTDDSHARGNWGLLDQMAALRWQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVS NKMRFLQLNFQRPDEEIIWSMSPVVDG VVIPDD
PLVLLTQGVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD
IVQDATFVYATLQTAHYHRET PPMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

FIGURE 92

GAGAACAGGCGCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
GCTGTCTCCTCGCTGCTGGGCGGGTCCAGGCTATGGATGGGAGATTCTGGATACGAGTCAGG
AGTCAGTGATGGTGGCGGAGGGGCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA
CAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC
CAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGAGAGGTGGAATAGACACCCGGGGCC
GATTCAGAGCTCACTGGGGATCCCGCCAGGGGAACTGCTCCTTTGGTGATCAGAGACGCGCAG
ATGCAGGATGAGTCAAGTACTTCTTTGCGGTGGAGAGGAAAGCTATGTGACATATAATTT
CATGAACGATGGGTTCTTTCTAAAGTAACAGTGCTCAGCTTCACGCCACAGCCCCAGGACC
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
GTCCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTATCAGCATTTACGTCGACAACAC
GCCAGCCTTGAGGCCACAGCCCCAGGAAATGTCCCATACCTGGAAGCCCCAAAAGGCCAGT
TCCTGCGGCTCCTCTGTGCTGTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTCTGCAG
AACAGAGTCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCCG
GGTGAAGGCTGGGGATTCAGGGCGCTACACCTGCCAGCGGAGAACAGGCTTGGCTCCCAGC
AGCGAGCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTTCCAA
GCAACAGGACAGTCTCGGAAACCTTGGGAACGGCAGCTCTCTCCAGTACTGGAGGGCCA
AAGCCTGTGCTGTGCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA
GGGACAGGTTCTGAGCCTCCAGCCCTCAGACCCCGGGTCTGGAGCTGCCTCGGTT
CAAGTGGAGCAGGAAGGAGATTACCTGCCACGCTCGGCACCCACTGGGCTCCAGACAGT
CTCTCTCAGCCTCTCCGTGCATATAAGAAGGGACTCATCTCAACGGCAITTTCTCCAAGCGG
CGTTTTCTGGGAATCGGCATCACGGCTCTTTCTTTCTGCTGCGCCTGATCATCATGAAG
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCCCAGGTTCTCCCGGCACAGCAC
GATCCTGGATTACATCAATGTGGTCCCGACGGTGGCCCCCTGGCTCAGAAGCGGAATCAGA
AAGCCACACCAACAGTCTCTCGGACCCCTCCTCCACAGGTGCTCCTCCCCAGAATCAAAG
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCCAAGACCCAAATCATCCACTCAAGC
CCCAGAATCCCAGGAGAGCCAAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA
GACCCAGGCTGAGGCCCGGATGCCAAGGGCACCCAGCGGATTATGCAAGAATCAAGTTCT
CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
GTTGAAGATAACAGAGTGCAAAAGTTTCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT
CTCTCTTTCTCTCTCTTTTAAAAAATCATCTGGCCAGGGCACAGTGGCTCACGCTGTAAATC
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCTGAGGTGGGAGTTTCGAGACCAAGCCTG
GCCAAGTCTGGTGAACCCCGTCTCTACTAAAAATACAAAAATAGCTGGGCATGGTGGCAGG
CGCCTGTAATCTACTACTTGGGAAGCTGAGGCAGGAGAACTCACTTGAACCTGGGAGACGG
AGGTTGCAGCTGAGCCAAAGATCACACCATTGCACGCGCCTGGGGCAACAAAGCGAGACTCCA
TCTCAAAAAAATAATCCTCCAAATGGGTTGGGTGTCTGTAATCCCAGCACTTTGGGAGGCTA
AGGTGGGTGATTTGCTTGAGCCAGGAGTTTCGAGACCAAGCTGGTGAACCC
ATCTCTACAAAAAATACAAAAATAGCTGGGCTTGGTGGTGTGTGCTGTAGTCCCAGCTGT
CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAAATGAGGCTGAGAC
TACTGGGCTGCATTTCTCAGACAGTGGAGGCACTTAAGTCAAGGATGAGACAGGAGGTCGG
TACACAGATACAGGTACATAAGACTTTGTCTGATAAAACAGATTGCAGTAAAGAGCCAAACCAA
ATCCCAACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCGTCTCACTGCTACACTCTCT
GACAGCACCATGACAGTTTACAAATGGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA
AAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAAATAGCAAGAAATAACCATAAAA
GTGGGCAACCAAGCAAGCTTAGGCGCTGCTCTTGTCTAGTAGGATGACCAATCTTTTGTTCCTT
TACTTTCTTAATAAACTTGCTTTACCTTAAAAAAA

FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPDLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYWFK
AVTETTKGAPVATNNHQGREVEMSTRGRFQLTGDPKAGNCISLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSTFPRPDHNTDLTCHVDFSRKGVSQAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPPWGPRPL
GLELPGVKAGDSGRYTCRAENRLGSGQRALDLSVQYPENLRVMVSQANRTVLENLNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRQKATFNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAAGTGTATTTACTGCTGCGTTT
 TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACTCTCAAACAAAGA
 AAGTCAAGCAGCGAGTGCATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
 TTTTGTACCAAGAGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
 CAATGGAACAATTCCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
 TTGATGAAGAACAGGTTGACATATATGCCATACAGAAGCTTGGATAGAGAGGAGCGATCCCTC
 TACATCTTAAGAGCCAGGTAATAGACATCGTACTGGAAGGCTGTGGAACCTGAGTCTGA
 GTTTGTGTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
 AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
 GCTGACGATCCCTCAAGTGGTAAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
 ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCAAATATGGATAGAGAAC
 TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
 TCTGGAACAACAAGTGATTTAATTAACTTTCCAGATGTTAATGACAATAAGCCTATATTTAA
 AGAAATTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
 TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
 GATTGCGAACAATTTGACATTATTACTAATCATGAAACTCAAGAGGGAATAGTTATTATTTAA
 AAAGAAAGTGGATTTTGAGCACCAGAACCCTACGGTATTAGAGCAAAAGTTAAAAACCTC
 ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTCCACCACTTCATTAAAGTCCAG
 GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGATATTGAAGTTTGTGA
 AGAACCACCAAGGGATCAATTGTAGGCGTGGTGTCTGCCACAGACCTCAGACAATAGGAAT
 CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCATATCAATGATAATGGTACAATC
 ACTACAAGTAACCTCACTGGATCGTGAAATCAGTGCTTGGTACAACTTAAGTATTACAGCCAC
 AGAAAAATACAATATAGAACAGATCTCTCGATCCCACTGTATGTGCAAGTTCTTAAACATCA
 ATGATCATGTCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
 GGTGAGGTAATCTCAGATATCAGTGCAGTGGATAGAGATGAATCCATAGAACAGCACCAATT
 TTACTTTAATCTATCTGTAGAAGACACTAACCAATTCAAGTTTTACAATCATAGATAATCAAG
 ATAACACAGCTGTCAATTTGACTAATAGAACTGGTTTTAACCTTCAAGAAGAACCTGTCTTCT
 TACATCTCCATCTTAATTTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCTTAC
 CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
 TGCCTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTGCATTATGATCATA
 TTTGGGTTTATTTTTTTGACTTTGGGTTTAAAAACAACGGAGAAAACAGATTCTATTTCCTGA
 GAAAGTGAAGATTTTCAGAGAGAAATATATCCAATATGATGATGAAGGGGGTGGAGAAGAAG
 ATACAGAGGCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
 CGGAAAACCAACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
 CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG
 CCCCTCCTTTTGATTCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC
 CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
 GGGACCTCGCTTTAAAGATTAGCATGCATGTTTGGTCTGCAAGTGCAGTCAAAATATAGG
 GCTTTTACCATCAAAATTTTTTAAAGTGCTAATGTGATTCGAACCCCAATGGTATGCTTTAA
 AGAGTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
 CTGAGTAATGATCTCATGGTTATTTTAAAGTCACTACATGCTGTCTGATTAACAGAGATGTG
 GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACAGATTTGAAGTAAAAATATG
 TAGGAAGATTAATAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATATAT
 CATTTATTACTTAGGAAGAAGTAAAAATACCAACGAGAAAAATTTAAAGGAGCAAAATTTG
 CAAGTCAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
 ATTGAAATGTATAGTCAGAGAAATTTTCATGAATTAATCCATGAAGTATTGTTTCCTTTAT
 TTTAA

FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQFVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLDNGNNSFYQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVSINDNEPKFLDEPYEAIVPEMSPEGLTVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTGVIIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLS
VNDNKPIFKESLYRLTVSESAPTGTSGITIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAFEPFSQYYETYVCENAGSGQVIQTISAVDR
DESIIEHHFYNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVDCDGSSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEBANTDPCAPPFDSLQTYAFEGTGLAGSLSSLESASVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 96

ATTTC AAGCCAGCCATATTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTTCGCAAACATTTGACATTATT

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCGCCCCGGGCGGGACCCCAACCCCGAC
CCAGAGCTTCTCCAGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCCTTAACCTTCCTCCGCGGGG
CCCAGGCCACTTCGGGGATCCGGGTTGCCCCACCTGCAAACTCTCCGCCCTCTGCACCTGCCA
CCCCTGAGCCAGCGCGGCCCCCGAGCGAGTCA**TGG**CCCAACCGGGGCTGCAGCTGTTGGGGC
TTCATTCTCGCCTTCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG
GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATTGACGAGGGGCTGTGGA
TGTCTTGCCTGTCGCGAGAGCACGGGCGAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT
CTGAGCAGCACTTGCAAGCAACCCGTGCCTTGATGTTGGTGGCATCCTCCTGGGAGTGAT
AGCAAGTCTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTGAAGACGATGAGGTGC
AGAAGATGAGGATGGCTGTCATTGGGGGTGCGATATTTCTTCTGCGAGGTCTGGCTATTTTA
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCCTATGACCCCACT
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCGC
TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCTCCCGAAAAACAACCTCTTACCCAACACCA
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGA**C**ACAGAGGCAAAAG
GAGAAAATCATGTTGAAACAAACCGAAAAATGGACATTGAGATGATCATTAACATTAGGAC
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTA CAAACAAACAAACAAACAAACAA
ACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAACTTATTTTATCTTCTTCTCTCA
ATATAGGAGGGGAAGATTTTCCATTTGTAATCTGCTTCCCATGGAGTAATCATACTCAAAAT
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTCTATTAAAA
ATAGACAGTAAAAATCACTTCTCATTATGTTGATACTAGCATCTTAAATATCTCTTAAAT
AGGTAATATGTATTTAATTCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCTGCC
TTATATACATATGTAACAGTCAAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCTTTTG
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTTCTTCAATTCTTCATGCGTGCCTTTT
CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT
TTGTTTTGTGTTTCTATTGGTCTCTATCTCCTGAATCTAACACATTTATAGCCTACATTTTA
GTTTTCTAAAGCCAAGAAGATTTATTACAATCAGAACCTTTGGAGGCAAACTTTCTGCAATG
ACCAAAGTGATAAATTCCTGTTGACCTTCCACACAATCCCTGTACTCTGACCCATAGCACT
CTGTGTTGCTTTGAAAAATATTGTCCAATTGAGTAGCTGCATGCTGTTCGCCCAAGGTGTTG
AACACAACCTTATTGATTGAATTTTAAAGCTACTTATTTCATAGTTTTATATCCCCCTAACT
ACCTTTTTGTTCCTCCATCTCTAATTGTAATTGTTTTCCCAAGTGTAATTATCATGCGTTTTA
TATCTTCCTAATAAGGGTGTGCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
ATCTGCTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT
TTCTATCTGCCAAATTGAGATAATGATACTTAACCACTAGAAGAGGTAGTGTAATTTAA
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTGGCT
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACAGTACCTTCATGTGATT
CACTGCCCTTCTCTCTACCACTGCTATTTCCACTGAACAAAACCTACACACATACCTTCAT
GTGGTTCACTGTCCTTCTCTCTACCACTGCTATTTCCACTGAACAAAACCTACGCACATAC
CTTCATGTGGCTCAGTGCCCTCTCTCTCTACCACTGCTATTTCCATCTCTTCAGCTGTGCTCT
GACATGTTTGTGCTCTGTTCCATTTTAAACAACCTGCTCTACTTTTCCAGTCTGTACAGAAAG
CTATTTCACTTGAGCAAGATGATGTAATGGAAGGGGTGTGGCACTGGTGTCTGGAGACCTTG
GATTTGAGTCTTGGTGCTATCAATCACCGCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATG
TTGTGGGGATCCAGTGAGATGAGAAATCACTGTAAGTGTGGTTTGTGAATTTAAAGAGTGCTAT
ACTAAGGAAAGAATTGAGGAATTAACCTGCATACGTTTGTGTTGCTTTCAAAATGTTTGA
AAATAAAAAAATGTTAAG

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI LAFLGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCVSQSTGGI
QCKVFDSLNLNSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDEVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQEFYDPMTPVNNARYEFGQALFTGWAAASLCLLGALLCCSC
PRKTTSYPTPRPYPKPAPSSGKDYV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCTATTGGGGGC
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAA
CNNTTCAACANTTCTATGACCCATGACCCAGTCAATGCCAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCT
GTTCTGTCCC

FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA
GGTGCGAAGATGAGGATGGCTGTTCATTGGGGGCGCGATATTTCTTCTTGAGGTCTGGCTA
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAGAATTCATGACCCTATGACCGA

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FIGURE 101

GGGCCCACCATTATCCAACCGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTCGCAGANACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTTCATTGGGGGCGCGATATTTCTT
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCTGCGA

FIGURE 102

ATTCTCCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTGCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTGGAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNNTTCNNGNNNTCTATGACCCTATGACCCAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTG
GGAGGTGCCCTACTTTGCTGTTCTGTCCC

	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1991	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100										

AGAGCACCCGCAGATCCAGTNCAAAGTCTTTGACCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCAATTGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT
GGTATGGCAATAGNATNNTTCGNGNNTTCTATGACCCCTATGACCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCCAGTGGCTGGGCTGCTGCTTCTCTCTGCCCTTCTGGGAGGTGC
CCTACTTTGCTGTTCTCTGCTCCCGAA

FIGURE 104

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCCTATGNTGGGGACAACATTGTGACNGCCC
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTTCATTGGGGGCGCGATATT
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA
ATTTTATGACCCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTNTTCACTG
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTCGGAACC

FIGURE 105

TCATAGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAGAATTNTATGACCCTATGACCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCINTTCACTGGNTGGGCTGCTGCTTCNTNNGCCTTNTGGGAGGTGCCCTA
CTTTGCTGTTCCTG

FIGURE 106

TTCTGGGATGGATCCGCCCCATCNCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC
CCAGAGCACCGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAGGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCAGTCAATGCCAGGTA
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

FIGURE 108

CGGTGCCGTAGCTCGCGGGGACCGCGGCTCGCCCTCGCCCTCGGCCCTGCGCCCTGCAC
CGGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCGTGCCCCG
ACCGGTCCCCGCTTTTTGTAAACTTAAAGCGGGCGCAGCATTAACGCTTCCCGCCCCGGT
GACCTCTCAGGGGTCTCCCGCCAAAGGTGCTCCCGCTAAGGAACATGGCGAAGGTGGAG
CAGGTCTGAGCCTCGAGCCGCGAGCAGAGCTCAAATTCGAGGTCCCTTACCGATGTTGT
CACCACCAACTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTAAAGGTGAAGACTA
CAGCACACGTAGGTACTGTGTGAGGCCAACAGCGGAATCATCGATGCGAGGGCCTCAATT
AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT
TATGTTTCAGTCTATGTTTGCCTCAACTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG
CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTGAATTGCCAGCAGAGAAT
GATAAACCATGATGTAGAAAATAAATAATATATCCACAACGTCATCAAAGACAGAAAC
ACCAATAGTGTCTAAGTCTCTGAGTTCCTTTTGGATGACACCGAAGTTAAGAAGGTTATGG
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAAGCAGTTCAAG
GAAGAAGATGGACTCGCGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTACGATTAGC
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTTCTTTA
TCGTTGGTGTAAATTATTGGGAAGATTGCCCTTGATAGGAGTAGCATGCACAGGATGGTAAATTG
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAAT
AATGTATGATGACATCTCACAGGTCTTGCCCTTAAATTACCCCTCCCTGCACACACATACAC
AGATACACACACAAATATAATGTAAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG
ATTGAGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAACCATGAGTAATGCCACAAT
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCCTTGGTACATGATGCTGGATTACCTC
TCTTAAATGACACCTTCTCTCGCCTGTTGGTGTGGCCCTTGGGGAGCTGGAGCCCAGCAT
GCTGGGGAGTGCAGTCCACACAGTAGTCCCAAGTGGCCCACTCCCGGCCCAAGGCTG
CTTCCGTGTCCTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT
TGACTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTAGAGATGTTTAAATGCATA
TTTAACCTATTATAATGATTTTCATCTCATGTTTTCTTATTGTCAACAAGAGTACAGTTAATGC
TGCGTGTCTGTAACCTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTATTGGGATGCTGGAGAAAGAGCTGCCA
GGAAGTGTTTTTCTGGGTGAGTAAATAACAACCTGTATAGGGAGGGAAATTCAGTAGTG
ACAGTCAACTCTAGGTTACCTTTTTTAATGAAGAGTAGTCAGTCTCTAGATTGTTCTTATA
CCACCTCTCAACCATTACTCACACTCCAGCGCCCAAGTCCAAGTCTGAGCCTGACCTCCCC
TTGGGGACCTAGCCTGGAGTACGGACAATAAGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
ACAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTCTAGTAC
TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGAACCAACCGAGTCTGTTTGA
CTATGTAGCATCTTGAAGAAGAAAAATATAATAAAGCCCCAAAATTAAGAAAA

FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFSTDVVTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID
AGASINVSVMQLQFFDYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRVFE
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE
NKQFKEEDGLRMKRTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCCTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTGAAAAGAAAAATTATAATAAAGCC
CCAAAATTAAGAATTCTTTTGTCAATTTGTACATTTGCTCTATGGGGGAATTATTATTTT
ATCATTTTATTATTTTGCCATTGGAAGGTTAACTTTAAATGAGC

FIGURE 111

TATTGTAAAGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNNTTCCTCGCCTGTTGGTGCTGGCCNNTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCGGTTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCTGCTTT
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAAGTCTTATTAGAGATGTTTAAATGCATATTTA
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAAGTCTGTTGGGTGAAGTGGTATTGCTGCTGGAGGGCTG

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FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTA AAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

FIGURE 114

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGTATTTCAGAGATGTTTAATGC
ATATTAACTTATTTAATGTATTTATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAACCNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCANTCCC
GGCCCAGGCTGCTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGAAATAAATGGCAGTGCTTTGTTCAANTT
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTCAATNTCATGTTTTCTTATTGTCACAAGGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC
CACGTGCCCCACTCCCGGCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA
CTGTTATTCAGAGATGTTTAATGCATATTAACTTATTTAATGTATTTTCATCTCATGTTTTC
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 117

GCAGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCCTCCGGCTCAGGCTGGCTGAGA
GGCTCCAGCTGACAGCGTCCCCCGCCGCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC
CTCGGGGACCAAAACAGCTTGGCAGGGTCTCACATTGTTGCGCAGGCTGGAGTTTCAGTGCCA
TGATCATGGTTTACTGACGCTTTGACCTCCTGGGTTCAAGCGATCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAATAATGCTGCTTTGGTTGATATTTTTACC
CCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
GGTACCCCGGATTGTTCAGTGAAAGGACTTTCCATCTCACCAGCCCGCATTTGAGGCAGATG
CTAAGATGATGGTAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCACTCCCAGC
CTTTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAAATGGCACC CGAACCTT
AACCAGGTTGAAAGTTCAAGATTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
TATCTGTTAGGAGAAAGACAGGTTGATGGCACCGACAGCAGGTTTCAGCATCTTGAGACAAA
AGGTTCTTAACCAATTTCCCTTTGAGCAGCTGTGAAGCTTCCACGGGCTGTAGTGGCAT
TCTCATTTCCTCAGCATGTTCTAACTGCTGCCCACTGTGTTTCATGATGGAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG
AAACGTGCGAGTTCTTAAGAGGACGAGGAGAGAAGCTATGTGGTGACCAAAGAGAGGGTAC
CAGAGAGCATCTGACGAGAGAGCGAAGGGTGGGAGAGAAGAAAAAATCTGGCCGGGGTC
AGAGGATTCGCCAAGGGAGGCTTCTTTCAGTGGACCCGGGTCAAGAATACCCACATTCCG
AAGGGCTGGGACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA
GCTGAAGCGTGCTCAGAAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA
TGCTTGGTGAATGATCCACTTCTCAGGATTGATAACGATAGGGCTGATCAGTTGGTCTAT
CGGTTTTGACAGTGTGTCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC
GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAAATGGAAGC
GCAAAATCATTTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCACCGGGGTTGAGAAGGAC
TACAACGTTGCTGTTTCGCATCACTCCCTAAAATACGCCAGATTTCGCTCTGGATTACGG
GAACGATGCCAATTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGATCATCTAAA
TCACAGAGAAAAACCGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCTCGGACTT
GAACTCTGTCAATAGCATTTCAACATTTTTCAAAATCAGGAGATTTTCGTCCATTTAAAAAA
TGTATAGGTGCAGATATTGAAACTAGGTGGGCACCTCAATGCCAAGTATATACTCTCTTTA
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT
AAACCTTCAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTTCTCAGGGTCC
TACTCTAAGAAGAACTCAATAGGATGCTGGTTGTGTATTAAATGTGAAATGCGATAGATAAA
GGTAGATTGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAAACAGCTTTGTACTA
CTCTGAGATGGATCCATTGAGCTCATGCCCTCAATGTTTATATTGTGTTCTCTGTTGGGCTC
GGGACATTTTAGTTTAGTTTTTTGAAGAAATCAAAATCAGAAAGAAAGCAAGCATTTAAAA
CAAAACTAAATAACTGTTTTACTGCTTTAAGAAATAACATTACAATGTGTATTATTTAAAAA
TGGGAGAAATAGTTTTGTTCTATGAAATAAACCTAGTTTGAAGATAGGGAAGCTGAGACATTT
TAAGATCTCAAGTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGTCATAGG
AAGACACTTCACAAATATGAATGATCATGTGTTGAAAGCCACATTTTTATGCTATACAT
TCTATGTATAGGTGCTACATTTTAGGACAAAGAAATCTGTAATCTTTTCAAGAAAGAGT
CTTTTTCTCCTTGACAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTTCTCTGATTAG
TAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTGVSVRRKRQV
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISQHVLTAAHCVDHGKDYVKGSKKLRV
GLLKMNRNKGSGKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCVSVDESNDLLYQYCDAESGSTGSGVYLRLLKDPDKKNWKRKI IAVYSG
HQWVDVHGVQKDYNAVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCGATTCTGATTCCGGCAAGG
ATCCAAGCAATGGAATGCTCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGAGGGGCCCTCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCAACCAGAAGCAGGTGATTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGCTAATGACCTGACAACCCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGGTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATCGCCTTGCTCTTAAAGGTCTGTACACTT
ATATCTGGAACCAAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTTGGACAATTCTAGTGTGGACTTCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATGTCAAGATTTCGTAACCTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCACGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC
TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGACATCCAGGGGCA
TGTCACCTTCAGTGGAAGAGTGAAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCAAAAAACAAGCCCCACATAAAAGAGGAATGCATCGTACCACTCCCTGCTATA
AACCCAAAGAGAAACTTCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTGAGGAGCCCTCGTAAGTTGTAAAGCAGAGCTGTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAGATTGATTAGTTTCAA
AAAAA

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAGWPWSECRTCGGGASYSLRRCLS
SKSCEGRNIRYRTCNSVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDFDNPCSLKCQ
AKGTTLVVELAPKVLGDTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDHLYLETCTLQGTKGENSELSSTGTFL
VDNSVDFQKFPDKEILRMAGPLTADFIKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCS
ATCGGGYQLTSAECYDLRSNRVADQYCHYYPENIKPKKLQECNLDPCFASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPEAKLPWFKQAQELEEGAAVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACCTCCCGTGGAGGGGCCGGTGGGCCCTCGGGCCTGAC
AGATGCGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG
GCCCCGCGTTCGTGGGGCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCGG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCCGAGGAG
GCGGCGGGTCAGCTCCGCGCGGAGCTCCGCCAGGCGCGGAGTGCGGCCAGAGCCTGGCGT
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGAGGG
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGAGTCTCTCAAAAGTTCAGCTCCAGCA
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAACTGGCTAACATTCTTTT
TACCAGGAACTAGCCCGCGCTTAGAAGGCACAAATGTACCCTCAATGTGTGTCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC
AATTTGGTGTGTCATGGGCTTTTTTCAAACTCCAGTAGAAGGTGCCAGACTTCCATTTATTT
GGCCTCTTCACTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGGGGATTGTAAAGAGGAAG
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTACTTGAAGAAAAAGAATTTTG
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTGGAGTTACTGAAAAATTATTTT
TGGGATAAGAGAATTTCAAGCAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA
GTACAATGAAAAATACAATTATATTGTAAATTATAACTGGGCAAGCATGGATGACATATTA
ATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC
CTGGTGTGTGCACACAAGTCTTACTTGGAATAAAATTTACTGGTAC

FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEAAAGQLRRELQAAECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLINNAGIFQCPLYMKTEDGFEMQFGVNHLGHFLLTNLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRLEGNTNVTNVNLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAAATAGGAA CAAGGAGTAAAGAGCTGTT
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT
TGAAGAAAAAGAAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
TTACTGAAAAATTATTTTGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGT CAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGT
TGTGTGGAATTATCTGCCTGGCTT

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTGGGCTCCCGAGCCAGCC
CTTTCCTAACCACCAACCTAGCCAGTCCCAGCCGCGCAGCGCTGTCCCTGTACGGAC
CCCAGCGTTACATGCATCCTGCCGTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACCTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAAATGCTGATGTTGCTTTAGTAAATTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCTTAAGGAAGAATT
TCCAAATGAAATCAAGTAGTGTTTGCCAGAGTTGATGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAATACCCAAACCTCAAATGTTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTGAGCGATCAGTGAAGCATTGGCAGATTACATCAGGCAACAAAAAAG
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCACTCTTGATCGCAGCAAAAGAA
ATATCATTTGGATATTTTGAGCAAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCG
AATATTTTGATGATGACTGTGCCCTTCTTCTGCAATTTGGGGATGTTTCAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGTTGTACT
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT
GTCCGAGAAATAACATTTGAAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAAGTTTAGAAATATTCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCTGTAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACTCAAGCAATTG
TATTTGACTTACATTCTGGAAAACTGCACAGAGAATTCATCATGGACCTGACCCAACTGAT
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAAACTTG
AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 125

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46927, pI: 5.21, NX(S/T): 0
MHPAVFLSLPDLRCSLLLLVTWVFTPVTTETSLATENIDRIINNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMKEYR
QQRSVKALADYIRQQKSDPIQEBIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERNILH
DDCAFLSAFGDVSKPERYSGDNI IYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFHMYVFGDFKDVLI PGKLKQVFVDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPRESSFQKLAPSEYRYTLLRDRDEL
```

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGT CAGCGATCAGTGAAAGCATTGGCAGATTA

FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCGNGGAGCCCCGGGTCGAGAGGACNAGG
TGCCGCTGCCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGGAGCCAGCCCTTTCCTAACCC
AACCCAACTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTNCGGANCCAGCGTNACC
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACAACCTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTGTTTTCAGTGAG
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCAATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAAACCTCAAATTTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAGCATTGGCAGATTACATCAGGC

FIGURE 128

GCCCACGCGTCCGATGGCGGTTACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTGGCACATTATGACATTTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCACTGTAATACCCCTGAATCCCTTGTAAGTCTCCAGAGTACCTCAT
CCACGCTTTCTTCTGTGTGATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCACTGATGAGTGGCCAGGA
CTCTATGACCCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTGAGAAGGAAGGATG
GTGCAAAATTAGCTTTTTATCTTCTAGCATTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTGTCTGTGGAAGACTG
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATAAAAA
GATTACCTCTGGTGTTGACAGGTTTGAAGTTGCACTTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCTAGTACATTGGAAGCTTTTGTTTATAGGAACCTTGTA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAGCGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATCTTAAGCATAAGTAAACATGATATAAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTATTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGTAAGGTATTCTTAAGAATTTGCAGG
TACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCTTTAGT
GCAATACAATAAACTCTGAAATTAAGACTC

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAAIIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLVDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

[illegible]

ATTATAGCATTTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCCTG
AATCCCCCTTGTA CTCCAGAGTACCTCATCCAGCTTTCTTCTGTGTGATGTTTCTTTGTGTC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCTCTTGGCATATCATATTGGAGGGTATA
TGAGTAGACCAGTGATGAGTGGCCAGGACTCTATGACCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTGAGAAGGAAGGATGGTGCAAAATTAGCTTTTTATCTTCTAGCATTTTT
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAAACACAGAAGAATT
GGTCAGTTAAGTGTGATCAAAAGGCCACCAAAAGGAGTCTTATCCAGCAAGATCCTGT
CCAAGAGTGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

FIGURE 131

CGGACGCGTGGGGGAAACCTTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACCTGGGGCTCCCGCCG
TGCTGTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTTGAC
TCGGTCTTGGGTGATACGGCGCTTGGCCACCGGGCCTGTCAAGTTGACCTACCCCTTGCACAC
CTACCCCTAAGGAAGAGGAGTTGTACGCATGTGAGAGGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAA'TGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTCCTCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCAATCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCCTATCTGCAATGAGAAATTCACAAGCGCACAGGAATTTCTTGAAGATGGA
GAAAGTGATGGCTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT
TGTCCTCTCGGTGATGGTATTGCTTTGGATTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTTGTGGTTGTTAGATCTAAACTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAAATCCACTCCTCATAGAGCTTTTAAATGGTTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAATAAAGTTACTCAATCTGTG

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847
<subunit 1 of 1, 323 aa, 1 stop
<MW: 36223, pI: 5.06, NX(S/T): 1
MAAPKGS LWRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYP
KEEELYACQRCRLFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHLLFPLTLVRSFWS DMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSY LQMRNSQAHRNFLEDGESDGFRLCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHREAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCAACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGTTGCCAGAATCAGCTGCCATTGCG
TGAAGTGAACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

100
90
80
70
60
50
40
30
20
10
0

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCCTGCTGCTGCTGACCATGGCCTTGCCCGAGGTTTCGGGGACCG
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTCCTAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

FIGURE 135

GCAGAGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGAGCTGCAATGGGCCGCGGCTG
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCGGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCATTTGATAGATTAAATAACTACAGGCCTTTCCCAAGACTACAAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCTCTTCT
GGAATGACATCAGCCAGTGTGAAGAAGGGA CTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTGATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC
ATTGAGTCCCTGAAGCTGAATATGTAGATTGTGCTTCTAATCTGAGCGCTACACTGGTTA
CAAGGGACCAGATGCTTGGAAAAATATGGAATGTCATCTACGAAGAAAACTGTTTTAAGCCAC
AGACAATTAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAAATGTGCATTTGAGTGAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAAATTTCAACGCGATTTGATGGAATTTTGACTGAA
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGATTTTCTCTACTTAATAGAACTAAGGCCTTT
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTCAACTCTTTACTGGAATAAAAAATTC
AGGATGAGGAAAAACAAAATGTTACTTCTGAAATACTTCATGAAATCAAGTCATTTCTTTG
CATTTTGATGAGAATTCATTTTTTGTCTGGGGATAAAAAAGACACAACTAAAGGAGGA
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG
AAATTGATAGCAAAATATGCCAGAAAGTGACCTAGTTATGAATTCATCTAACAGACAAGA
AATAGTATCATTTATCAACGCATTTGGAAGAATTTCTACAAGTGTGAAGAATTAGAAAACT
TCAGGAACTGTTACAGAATATTCATTAAAGAAAAACAAGCTGATATGTGCCTGTTTCTGGAC
AATGGAGGCGAAAGAGTGGAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATGTTTTAAGTAAACACATTTTT
AAAAATGTGTAAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTTAAATATTGAATAAAAGGAGGATTATCAATTTAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974

<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLGAVLLSSGHGEEQPPETAAQRCFCQVSGYLDCTCDVETIDRFNNYRLF
PRLQKLLSDYFRYYKVNLRPCPFWNDISQCGRDCAVKPCQSDVPDGIKSASYKYSEE
NNLIEECEQAERLGAVDESLEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAF
YRLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRLSKVLPPFFERPDLFTGNKIQDEENKMLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYE
FHLTRQETIVSLFNAPGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAAACTGTTTTAAGCCACAGACAATTAAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACATTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAAGAAATGGGGACACA
ACATTACAGAATTTNAAACAGCGATTTGATGGAATTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAAGTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCCAGATTTTCAACTNNTTACTGGAAATAAAATTCAGGATGAGGNAAACAAA
TGTTACTTTTGAAAATCTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATTCA
TTTTTTTGCTG

FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA
AGTGAAGAAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC
CGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCCTGGTGTTCCTGACAGG
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC
GCCCCCTGGGATGGGCTTCAGGCGACCCGAGGGGGGACGTTTTATCGCTGCCCTGTAGGGGG
GGCCCCAATGCCCTATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC
ATCTGTCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC
ATGGTGAGCTAAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGGAAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCTAGAAAGCAAA
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCCAAGCTGGGAGTAACTATTTCCCCATCCCCAGGCCCTGTGCCCTCTCTGTGCTC
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCTGCCCCAAGCTGAGCCAGAGGAAGGCTGAGTACTTGGTT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGC AAAAGCTCCATGTTTCTTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTCAAGAGTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ATCTACTCGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG
AGCCAAGATTGTGCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAAATTAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGAGGAGGATTGCTTGGGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAATAAATGTTTTAAAAAT

FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSFNLDEHHPRLLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW
DGPSGDRRGDVYRCFVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

FIGURE 140

CACAGTTCCTCCACCATCACTCCTCCCATTCCTTCCAACCTTTATTTTATAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCTTCGTCACCTCACCTGTTCTTG
CCCTTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAAGCTGAATTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAACTGGGAAATTCACTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTAGAGA
CAGATGGTGATGG

FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCCCCTTTCTGAGCTTCTCTGGGCCGGCTCTAGAACA
ATTTCAGGCTTCGCTCGGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATCCATGTTTGTCTCAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCTGGAGA
AACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTCTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCAGACCTCAGCCTG
GAGCATCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTGGCCTACTGGAGGAGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
GGGTATTCCAGTGCACTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT
GGTCGTGCCACTGTTCTGTCTGGAATAATGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
TGGTCTCCAGACACCTTGAATAAATCAACCTTACCCAGAAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCGTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
CTCATAGGTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGTCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
TACACCCAGCACTTGAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTCTAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGAGAGCCCCACTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGCCCACTGAAATGGGATGTGCATGAACACGGAGGATC
CATGAACACTGTAAAGTGTTGACAGTGTGTGACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTCAGCAATAAAAAGGCCACCCTGGCCAAAAGCGGTAAAAAA
AAAAAAAAA

FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEBIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIA
PGETVYYSVEYQGEYESLYTSHIWIPISSWCSLTEGPECVTDITATVPYNLRVRATLGSQTS
AWSILKHPFNRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGAEEHV
KMVRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVQGEAIPLVLALFA
FVGFMLILVVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACAT
AVMSPEELLRWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGCCATTCTGC
CTGCCCCTCAGAACCCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 144

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCGGGAAAAGAGCAGAGGAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTTGGGGAATGGGACTCCCTGTGGGAGGAGAGAAAGCTGGAAGTCCCT
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGC
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGTACAAGGATAATCTCCAGGGAACCTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCTGCCTGCACCCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCTCCTTTACAGCCACCGACTCAGTGAAGTGC GGCTGCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGTG
AGGTGCAGCTCATTCACTTCAACCAGGAACCTTACGGGAATTTACGCCTGCCTCCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCTT
CAGTCGCCCTCCTTAACCGCGACACCATCACTCGCATCTCTACAGAATGATGCCTACTTTT
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGACCCCGCCTGCTCCGAGACTGTCACTGGATCTCATTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCTCCATCTCAGATCT
TCCAGAGCCTCAGCGTAACAGCCGGCCCCCTGCAGCCCTTGGCCACAGGCACTGAGGGGC
AACAGGGACCCCCGGCACCCCGAGAGGCGCTGCCAGGCCCACTACCGCTGCATGTGGA
TGGTGTCCCCATGTCGCTGAGACTCCCTTCGAGGATTGCACCGCCCGCTCCTAAGCCTC
CCCACAAGCGAGGGGAGTTACCCCTAAAACAAGCTATTAAAGGACAGAATACTTA

FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGKELRGTLTYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLFLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFLSRLLNRDTITRISYKNDAFLQDLSELELLFPESFGFITIQGSLSTPPCSE
TVTWILIDRALNITSLQMHSRLRLSQNPSPQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

FIGURE 146

GGCGCCTGGTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGGCCGACGCTCCGCGCCGAGCCTC
GTTCTGCTCCCGCCCTCGCTCTGCGAGTACTGCTCAGAAACGCTGGGGCCGCCACCTTCGCGAGACTAACGAA
GCAAGTCCCTTCCGCCCAACCACTCGAGGTCATTAATTTGGACGCTTTGCTGCCATTTCTCCAGGTTTGAGGGAGC
CGCAGAGGCGGAGGCTCGGTATTCCTGCACTCAGCACCCAGCTCGCCCCGAGCGCTCGGTGCTCAGGCCCTTC
GCGAGCGGSGCTTCGGCTCGCGTCCCTTGTGAAGGCTCTGSGCGCTCAGAGCGCGGCCGCTCGGTTTGGCT
CACTCTCCCGAGAACTTCACTGCGAGAGCCAAAGGAGTGGGAAGAGCTGTCTTGGAGATTTTCTGGGGA
ATCCTGAGGTCAATCATTTATGAAGTGATCCGCGCGGGAGTGGCTCAGAGTAACCAAGTGTCTGTTATGGCTAGA
GCAATTCAGCCATGGTGGTTCCTCAATGCCACTTTATGGAGAACTTTGGAAAAATACATGGGATGGGATGGT
GAGTGGTGGATAGCAAAACAGCAGGGGAAAGGGCCATCAGAGCAATGACATGCGAGAGTATTTGGACCTTCAT
AATAAATTACGAAGTCAGGTGTATCCAAAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAGA
TCTGCAAGATCCTGGCTGAAAGTTGCTTGTGGGAAATGAGACCTGCAAGCTTGTCTCCATCAATTGGACAGAAT
TTGGGAGCACATCGGGGAAGATATAGGCCCGGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAGACTTT
AGCTACCCATATGAACATGAATGCAACCCATATGTCCATTCAGGTGTTCTGGCCCTGTATGTACACATTAACA
CAGGTGCTGTGGGCACTAGTAAACAGAATCGGTTGTGCCATTAATTTGTGTACATGAACATCTGGGGGCG
ATATGGCCCAAGCTGTCTACCTGGTGTGCAATTACTCCCAAGGGGAACTGGTGGGGCCATGCCCTTACAAA
CATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTGGAGGGGCTGTAGAGAAAACTGTGCTACAAAGAGGG
TCAGACAGGTATTAATCCCTCGAGAGAGGAGAAACAAATGAAATGAAACGACAGCAGTCAAAAGTCCATGACACC
CATGTCCCGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAATGTCCCAAATGTTTCT
TGTGAAGTAAAGTTAAGAGATCAGTGTCAAAGGAAACAACTGCAATAGGTACGAATCTCTGCTGGCTGTTGGAT
AGTAAAGCTAAAGTTATGGCAGTGTCATTTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
ATAATAGACAAATGATGGTGGCTGGGTAGATATCACTAGACAAAGGAAGAACCTATTTTCATCAAGTCCCAATAGA
AATGGTATTCAAACAAATGGCAATATCAGTCTGCTAATTCCTTCAAGTCTTAAAGTAAACAGTTTCAGGCTGTG
ACTTGTGAACCAACTGTGGAACAGCTCTGTCCATTTATAAGCCTGCTTCAATTTGCCCAAGAGTATAGTCTCCT
CGTAACTGTATGTCAGAGCAATCCACATATGCTCGTGTAAATGGAACTCGAGTTTATCTGTATCTGTCCAGTATC
TGCAAGACAGCTAGTACATGCTCGAGTGGTTCGAAATCAGCGTGGTTATGTTGATGTAATGCTGTGGACAAAAGA
AAGACCTACAGTCTCTTCTTCCGAATGGAATCTTCTCAGAAAGTTTACAGAATCTCCAGGAGGAAAGGCAATTC
AGAGTGTGCTGTGTTGTGGAACCTGAATACTTGAAGAGGAGCCATAAAGACTATTCCAAATGCAATATTTCTGA
ATTTTGTATAAAACCTGAACCTACTGTACAGAGTACATCACTATTTTCAGCCCAAAAGGTCGCAATGCAATA
TAAATCTGTATAAACAAGCTCTATAAAATAAACAATGGGACATAGCTTTTGGGAAAAGTAAATGAAAATATAATGG
TTTATGAATCCTGTGTATAATATGTCTATATTTCTTAGCAGTTATTTCTACAGTTAATTAACATAGTCATGATT
GTTCTACGTTTCATATAATATATGGTGTCTTGTATATGCCACTAATAAAATGAATCTAAACATGAAATGTAAATG
GCCCTCAGAAATCATCTAGTGCATTTAAAAATAATCGACTCAAAACTGAAAGAAACCTTATCACATTTTCCCC
AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAAATAATTTTCCACTTAATAAGTGTAAAGTTTTTTTC
TGTAAATTTAGGCATATAGAAATATAAATCTGTATATGCACTTCTATTTTATATAAAATTAATCCTTTAATATC
CAATGAATCTGTTAAAAATGTTTGTATTCCTTGGGAATGGCCTTAAAAATAAAATGATATAAAGTCAGAGTGGTGGT
ATGAAACATCTCTAGTATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTCTATGTACTGTATA
AATTTGAGTGACATATTTTCTTTGTATCCTGGCAAAATACCTCTGAGGCCAGGAAGTATAATAGCAAAAAGTT
GAACAAAGATGAACATAATGTATTAACATTAACATGCCACTGATTTTTTTTAAATGGTAAATGACCTTGTATATAA
ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTCTATGAAAAATGTATTGTGGCTTTGATACATAA
AATCTGTAATAATGTTAGTTTGTGTAATTTTCTGCTGGTGGATTACATATTAATTTTTCTGCTGGTGGGA
TAAACATTAATAATTAATCATGTTTCAAAAAA

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTLVFMARAIPAMVVPNATLLEKLEKYMDEGGEWWIAKQRGKRAITDNDM
QSILDHLNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW
GRYRPPTFFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGVPVCTHYTQVWATSNRIGCAINLC
HNMNIWGQIWPKAVYLVCNYSKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCKEGRSDRY
YPPREETNEIERQQSQVHDTHVTRSDSSRNEVISAQMSQIVSCEVRLRDQCKGTTTCNR
YECFAGCLDSKAKVIGSVHYEQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI
QTIGKYQSANSFTVSKVTQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCGCGGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCAAGCGCG
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGTGCTCTGTGCTGCTGGCGGTGT
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCGGAAGGGACCCAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGTTAT
CATCACCAACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC
AGAGCACCAAGCGCTTCATCAAGTGGTACACGCCTGGAACGAGAAGCGCAGGGTCTACGAA
GAATAGGGTGAAAAACCTCAGAAGGGGAAAACTCCAACCAGTTGGGAGACTTGTGCAAGGA
CTTTGCAGATTAAAAAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCAGATGGGAGACCCATCTCTCTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACTCATGCCCTTCCCTTTTAA
AAAATGCTTTTTTGTATTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCCGGGA
GGAACAATGAGCTTGGTGGACACATTTCAATGCAAGTGTGCTCCATTCCTGAGCTTGGGAAGC
TTCGCTTAGAGGTCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT
GGTTAATTTTACACACCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACTGTGAGCAAAAAACCTTAGGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA
AACCTTCAAAGCATGTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTCCCATGTAAATCTTCAATGTTAAACAGTGCAGTCTCTTTTGAAGCTAAGAT
GACCATGCGCCCTTTCTCTGTACATATACCCCTTAAGAAGCCCCCTCCACACACTGCCCC
CAGTATATGCCGATTGTACTGCTGTGTTATATGCTATGTACATGTGAGAAACCATTAGCAT
TGCATGCAAGTTTCATATTCTTTCTAAGATGGAAGTAATAAAATATATTTGAAATGTAAAA
AAAAAAAAAA

FIGURE 149

MSLLPRAPPVSMRLLAALLLLLLALYTARVDGSKCKSRKGPKIRYSDVKKLEMKPKYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNAWNNEKRRVYEE

Signal sequence:

amino acids 1-34

FIGURE 150

GCCCAGGGACTGCTATGGCTTCCTTTGTTGTTTACCOCGGTCTGCGCTATGTTAAACTCCAATGTCTCCTGTG
 GTTAACTGCTTCCTGGCATCAAGTTTCAACCTCATTTGACAGCCCAAGCAGATATCCAGTTGTCAACACAAATTTATGG
 CAAAATCCGGGGCTTAAGAACACCGTTTCCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTTAGGGGTCCCCTA
 TGCTTCAACCCCCACTTGAGAGAGCGGGTTCAGCCCCAGAACCCCCGTCTCTCGACTGGCATCGGAATATAC
 TACTCAGTTTGTCTGTGTGCTGCCCCAGCACCTGGATGAGAGATCCTTACTGCTATGATGCTGCCCCATCTGTTT
 TACCGCCAATTTGGATATCTTTGATGACCTATGTTCAAGATCAAAATGAAGATCGCCTTTACTTTAAACATCTACGT
 GCCCAGGAGAGTGGAGCCAAACAAAGAAAAACGAGATGATATAACAGGTAATGACCGTGGTGAAGACGGAAGA
 TATTTATGATCAGAAACAGTAAGAAAGCCCGTCATGGTCTATATCCATGGGGGATCTTACATGGAGGGACCGGCA
 CATGATTTGACGGCAGCATTTTGGCAAGCTACGGAACGTCATCGTGATCAACATTAACTACCGCTCTGGGAATACT
 AGGGTTTTTAAGTACCGTGAACGAGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCATCTCGGTG
 GATTGAGGAGAAATGTTGGAGCGCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCCTC
 CTGTGTGACGCTGTGTGACCTGTCCCACTACTCAGAAAGTCTCTTCCAGAAAGGCATCATTAGAGCGGCGACCGC
 CTGTCTCAGCTGGGCACTGAATACAGCGCGGCCAAGTACACTCGGATATTGGCAGACAAAGTCTGGCTGCAACAT
 GCTGGACACACGGACATGGTAGAATGCCGTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC
 GGCACCTTACCACATAGCCTTCCGGGCGGTGATCGACGGCGACGTCATCCAGACGACCCCCAGATCTCTGATGGA
 GCAAGGCGAGTCTCTCAACTACGACATCATGTGGGCGTCAACCAAGGGGAAGGCCCTGAAGTTCTGTGACGGCAT
 CGTGATAACAGGAGCGGTGTGACGCCCAACGACTTTGACTTCTCGTGTCCAACTTCTGTGACCACTTTACGG
 CTACCTTGAAGGGAAAGACACTTTGCGGGAGACTATCAAGTTTCATGTACACAGATGGGCGGATGAAGGAAACCC
 GGAGAGCGGGCGGAAACCCCTGGTGGCTCTCTTACTGACCCAGAGTGGGTGGCCCCCGCGCTGGCCGCCGACT
 GCACGCGCAGTACGGCTCCCCACCTACTTCTATGCTTCTATCATCACTGCGCAAGCGAAATGAAGCCGAGCTG
 GGCAGATTCGGCCCATGTGTATGAGGTCCCCATGTCTTGGCATCCCCATGATCGTTCACCGAGCTCTTCAG
 TTGTAACTTTTCAAGAAGCAGCTCATGCTCAGCGCGGTGGTCTGACCTATGAGCAAGCTTCGCCAAAAGTGG
 TGATCCAAATCAACAGTTCTCAGGATACCAAGTTTCATTACACAAAACCCAGCCGTTTGAAGAAAGTGGCGTG
 GTCCAGTATAATCCCAAGACAGCTCTATCTGCATATTGGCTTTGAACCCAGAGTGAAGATCACTACCGGGC
 AACCAAGTGGCTTTCTGGTTGAACCTGTTCTTCTATTGCAAACTTTGAACGAGATATTCACGATGTTTCAAC
 AACCACCAAGGTTCTCTCAGACAGCATGACATCTATTCCCTATGGCACC CGCGCATCTCCCGCAAGATATGGCC
 AACCACCAACGCCGAGCAATCACTCTCTGCCAACAAATCCCAAGCACTCTAAGGACCCCTCAAAAACGGGCTGA
 GGACCAACTGTCTCTCACTCACTTAGCTTTTGGCGCGCTGTACTACAAAAGGACAAGAGGCGGCATGAGATCAAG
 GCGCCCGAGTCCCAGAGAAACACCAAAATGATATCGCTACATCCAGACAAGAGATCATGTCTGCGAT
 GAAGCAGCTGGAACACGATCACAGAGTGTGAGTGCCTGAGGCACACGACACATGAGCTCACCTGCCCGCGAGA
 CTACCCCTCAACGCTGCGCGGTCGCCAGATGACATCCCACTTTATGAGCGCAACACCATCACATGATTTCAA
 CACACTGACGGGATCGAGCCTTTGACACTTTTAAACCTTTCACTGGAGGACAAAACAGTACAAATTTACCCCA
 CGACATTCACCACTAGAGTATAGCTTTTGGCCCTATTTCCCTTCTATCCCTCTGCCCTACCGGCTCAGCAACAT
 AGAAGAGGGAAGGAAAGAGAGAAGGAAAGAGAGAGAGAAGAAAGTCTCCAGACCAAGGAATGTTTTGTCCCACT
 GACTTAAGACAAAATGCAAAAAGGCGAGTCACTCCATCCCGGCGAGCCCTTATCGTTGGTGGTTTCCAGTATTAC
 AAGATCACTTCTGACCTGTGAAATGTGAGAAGTACACATTTCTGTTAAATAACTGCTTTAAGATCTCTACCA
 CTCCAATCAATGTTTAGTGTGATAGGACATCACATTTCAAGGCCCGGGGTGTTTCCAACGTCATGGAAGCAGCT
 GACACTTCTGAAACTCAGCAAGGACACTTGATATTTTAAATTACATGGAAGTTTAAACATTTCTTTCTGTGTC
 CACACATGGATGGCTCTCTTAAAGTGAAGAAAGAGTCAATGAGATTTTGGCCGACATGAGAGCTGTAATCCAG
 AGAGAAGGAACGTAGAAATTTATTTAAAGAATGGACTGTGACGCGAAATCTGTACGGTTCTGTGCAAAAGAG
 GTGTTTTCGACGCTGAACATATTTTAAAGACTTTGT

FIGURE 151

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVVPYASP
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLPWFWTANLDTLMTYVQDQN
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDAQAKGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLTLTSLHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCNML
DTTDMVECLRKNKYKELIQQTITPATYHIAFGPVIDGDVIPPDPQILMEQGEFLNYDIMLGV
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIFMYTDWADKENP
ETRRKTLVALFTDHWAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVFPYV
FGIPMIGPTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPVQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPPDMTS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTELSVTTIAVG
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLRLTCCPPDYTLTLRRSPDDIPLMTPNTITIMIPTTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTACTCTCTTTCTTTTGTGGGTCGTGGCAGGGGCCA
CAGCAAGTCCGGGCGGGTCAACCGTTGAGTACTTGAACCGGAGCACTCGCTGTGCAAGCC
CTACCAAGGTTGTGGGCACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGATATATCCCGCTTACCCCAGATATGCAAGAGTAAACAGGGTGCCCTGTGGAACCGG
GTGCCATGTTTCTGAGAGACTGGGAGTTGAGGTGCATCTCAAATCCAGTGCACGAAAGGAA
GAAGAACTCTGCATGGGGATGGCTTGCCAATCTGTGATCAAAAGGATCGGATCAGCCAGGGCC
CTGTGTTTGGAAACATGGACAATTTGTGGGGCTGGGAGTATTTGTAGACATACCCCAAA
GAGGAGAAGCAGCAAGAGCGGGTATTCCCTACATCTCAGCCATGGTGAACAAACGGCTCCCT
CAGCTATGATCATAGAGCGGGATGGGCGGCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTATTACACACCTTCTGGTGTATCGCTAGCTCAAGAGCATTGACGATAATGT
ATGGAATCTGATGGCAAGCATGATGAGGAGGAGCTGCATTGAAGTGCCCGGAGTCGCGCTGCC
CCGAGGTACTACTCTCGGCACCTCTCCATCACTGGGAGTCTCATAGATACTCATGATGCA
TTTCTTGAAGTTGTTTGAATGCAGTGGAGAGAACCCGCAAGAGGAAAGACTCCATCGA
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGTGCCTGAGATGACAGCTCCATCGGCCGC
CTCAGATGGCCCTGGCCCTCTTCTCATCGTCTTTTCTCCGCTGGTGTTTCTGTATTGGCA
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA
GCCCTCTGCTGCTGCCACCACTTTTGTGATGCTACCCATGAGGTATGGAAGAGCAGGCATG
GCTTGAGCATCGAGCCTGGAGAGTGTCTTGTCTTAGCAGCTGGTTGGGGACTATTCTGT
TCACTGGAGTTTGAATGCAGGGAACCCCGCATTCCTCATGGTTGTGCATGGGGACATCAAC
CTGTGCTGGGAAGCCACCCACCGGGAATGTCTGTGTGATGTGCCCTTCCCTGAGTCC
TTCCATGTGGGAGCAGAGGTGTGAAGAGAAATTAACGTGGTTGTGATGCCAAATCAGAGC
AGAATTTCCATAGCCGAGGCTCGCGTGTGTTTGTGATCAGAAGCCCTTCTACTTGCAATTTG
AATCCACAAAGAAATAAAACTGGTAAACACAGGCCTTTTGCACCTCATTCGTTGGGTT
TTGCATTGACCCAAACCTCTGCCTACCTGAGGAGCTTCTTTTGGAAACAGGATGGAACCT
TCTTCTGCTTACCTTCTCTTTTCACTCCATTCATTGTCTCTCTGTGTGCAACCTGAGCT
GGAAGGCAATTTGATGCCCTCTCTGTGGGGCTGGGGCTGAGAAAGCAGCTCGGTTTAC
TGGCCTTCACTTAGGTGGCCCTAGGAGATGGCTTCTGTGTTGGATCACTGTTCTCCCTAGCAT
GGGCTTGGGTCTATTGGCATGTCCATGGCCCTCCCAATCAAGTCTCTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACCACTCAGGTTTGTATCAAACCAAAGCAACATTTGTCACTGTG
GTCTGACATGTGGAGATGTTTGTGCACTTGTAGAGCTGTAGCTGTAGCTGTGATGTTTGTGAT
TACGATTTTGGAAATCCCACTTTGAGTGTGTAAGTGTGAAGGAGCTTCTTCTTACACCTT
GGGCTTGGATATTTGCCACAGAGAAGAAATTTGGCTTTTTTTTCTTAAATGGCAAGAGCAGT
TGCTGTTCTCATGTTTCAAAGTTGAGAGCAACAGACCTTCATCATCTGTGCTCGGAAGAGT
CATGTTGATTGAGCAGCAGCAGCTGATGCTGGCCCTCTGTCAACCTTATTCCATCGGCTTAT
TTTGAACAAGGGTTACATGCTGCTCACTTACTGCTGCTGGGATTAATCAGTTACAGGCCAG
AGTCTCCTTGGAGGGCCTGGAACCTCTGAGTCTCCTATGAACCTCTGTAGCTTAATGAAAT
CTTAAATACACCGATGGAACCAAATAAAATAAAAGGGCGGCGCGCACTTACGAGTGTG
ACCTTGCAGTAGGGATCAACGGGTAAATAGCTTGGCCGCACTGG

FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFVKIHGQGKKN
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDYTPNEEKQQERVFPYISAMVNNGSLSY
DHERDGRPTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKLFEVERTPEEEKLHRDVFLLPSVDNMKLPENTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

FIGURE 154

CCGAGCCGGGCGCGCAGCAGCGAGCTGGGGCCGGCCTGGGACCATTGGGCGTGAGTGCATCTACGGATCAGTCT
CTGATGGTGGGTGCTTAACTCTAGTGGGACTCCAGATTCCATGAAGAAAATCAGTTGTCTTTCATTCAAGAAT
TGGGGTCTTAAGAAATGGAATGAGTAGCAAGAGTCGAAAGAAATCTGTTTCTAGAAGAGGTTTAAATTAATGCTCGAGTCT
GACATGTTCCCGATTTCAGGTGAAACCATGAAGAGAAAATAGAATACTTAAATATGCTTTTCCGCAACCGCTTCT
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCTTTGTGAGCCTCAGCCTCGAGTCTTCCACCTGATCCCGGTGT
CGACTCTTAAGAAATGGAATGAGTAGCAAGAGTCGAAAGAAATCATGCCGACCTGTGACCGGAGCCCTGTGGA
CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCAAGTGTGGCCGAGCGCAGCATGGAAGGTTCATGCCCC
CGATCATTTTAAGCTGGTCTCAGTGATGTTTATTGCCACGGAGACAGGTACCCACTGTATGTCTATTCCCA
AAACAAAGCGACAGAAATTCAGTGCATCTGGTGGCTAACAGGAAACCGTATCACCCAAACTGGGAAGCTTCA
TTAGTCACATGTCAAAAGAGATCCGGAGCCTCTTTCGAAAAGCCCTTGAACCTCCTTGGCTCTTTTACCCAAATCAC
CATTTGTGAGATGGGAGAGCTCAACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTTCAGCTGCTGAGGGATA
TCTATCTAAAGAAACCAAACTCCTGCCCAATGATTGGCTGCAGACAGCTCTATTTAGAGACCCTGGGAAAC
GCCGACCCCTACAAATGGGCTGGCCTTGTCTTATGCTTCTTCCAGATTTTGACTGGAAGAGATTTATTTCA
GGCACCAGCCAAGTGGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAAGAACAGTATCTGGAAAAGGAGC
AGCGTCGTGAGTCTCCTACGTTTGAAGAACAGCCAGCTGGAGAGAACCTACGGGGAGATGGCCAAAGATCGTGG
ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCCAATGTGAGCT
TTCCTGTACAGAAATGGCTGTGTGACATGGAGCACTTCAAGGTAATTAAGACCATCAGATCGAGGATGAAA
GGGAAGACGGGAGAGAAATGTACTTCGGGTATTCTCTCGGGTGGCCACCCCATCCTGAAACCAACCATCG
GCCGGATGACGCTGCCACCGAGGCGAGGAAAGAGAGCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGT
CACCAGTTCTCAGTGCTTGGGCTTTTCAAGGCCAGGTTCCCAAGGTTTGACGCCAGGTTGATCTTTGAGCTTT
GGCAAGCAGAGAAAAGCCAGTGAACATTCGCTCCGATTCTTTACAATGGCGTCGATGTCACTTCCACACT
CTTTCTGCCAAGACCACCAAGGCTTCTCCAAGCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAAA
GGGACATGTTGTAGCCCTGGGAGGAGTGTACAAATATTATGATGATGTACAGGGAAGGATTCTAAAGG
GAGCGTACAGCAGTATAGATCCATGCCAATACAGAGCATAGGGAAGGTCCACTTCTGTTTGTGCTGTTAC
TAAGGCTAGAAGATTATGCTTTTAAAGGCTAAATATTGTTTGTGGGAACACAGATGTTGGGGTGTGAACAGT
AAGCATGTTCTGCAATGTGGTACCTGAATGCTTGGTACAAAATGAGGCGAGTACAGAGGAATAGAAGGTACTT
TATCATGCGAGACTCTGCTTAGAATGCCAGAAATAATAGTTCAAGACCTGAAGTGGCCATCCAGATTGTGAC
TCTTCTGGCTGGCCCATGTTACTATGATGGAACACAGCACACTCAACAAAATTTTTCATCTTAGACATT
TTTCAAGCCAGTTTGAATGACTCTTATCTGATGATTTATCTAAATTAAGGTTGGCAACTTTTTCTGTAAAG
GCCAGATTGTAATAATTCAGACTGTGTGGAACAAAAGGCCACATACAGTCTCTGTCACTACTCAACTCTGT
TTCTGAAGCAGGAAAGCCACAGACAGTACATAAAGGAATATGTGTAGTGGGTTCAGGCGCAGACAAAC
GATGGTGACAGACTTGGCCCTGGGCTGTAGTTTGTCTAGCCCTCATCTAAAAAATAGGCTATACTACATTC
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTCTCCAGTACTCTGCTAGAAAC
CAGAAATTTGGTCTGTATCTGACACTAGAACAAAATTCGAGGGTAAATAAACATTGAAATAGAATGAATCATAGAA
AATGATTAGAAGAATACTTGATGTTTATGATGATTGTGATACAGATAGTTTAAAGTATGTTCTAAATATTGTT
CTGCTGTAGTCTATTGCTGTATATGCTGAAATTTTGTATGCCATTTAGTATTTTATATGTTTAGGAAAAAT
TTCTAAGACCAAGTTTGAATGACTCTTATCTCTGTAGTAATATTCAATTTGCTGTACCTGCTGGTGTAGAAG
GAGGCTAGAAGATGAATCAGGCACTTCTTCCAATAAACTAAATATGCTCATTTCCCTTTGACAGCTGTAGA
ACTGGATTCAATTTTAAACCAATTTTCACTAGTTTCAATGGTAAATCTGATTGATTTTAAATGCGTTTTTGA
AGAATTTGCTATTAGGTAGTTTACAGATCTTTAAGGTTGTTTATATATTAGAAGCAATTAATATTACATCTG
TGATTTCTGAACTAATGGTGCTAATCTCAGAGAAATGGAAAGTGAAGTGAGATTCTCTGTGCTCCGCAATCC
AATCTTTCTCTTTGTTTTGTCCAGTGTGCAATTAATGATGCTGTTCTATAAATAAATTTTTTAAGAATAA

FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLALLAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDVPTEPPVTDVPVY
EALLYCNIPSVASERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMCHFCHNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLGAHPILNQITIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPFAARLIFELWQDREKPSSEHSVRILYNGVDVTFHTSF
CQDHHKRSPPKPMCPLENLVRFVKRDMFVALGGSGTNYDACHREGF

Signal sequence:

amino acids 1-18

FIGURE 156

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCCTTTTGAAGAACAGTACTGTGGGA
 GCTATTTAAAGAGATAAAAAAGAAATATCCTTTCTGGGAGTTCAGAGATTGTGCAGTAATTTGGTTAGGACTCTGAGC
 GCCGCTGTTCAACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGCAACGCGCTCGAAGCACAAAGCAGAT
 AGCTAGGAATGAACCATCCTCGGGAGTATGTGGAAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTTCTAT
 GGGCGAAGGACTGCTCCTGACTTCACTGGTTAAGGGCAGAATTGAAAAATTAATCTGGAGGAAGATAAAGATTGAT
 TCCTGCGCGACTGCAACGGGACTACAAAGGGCTTGTCTGCTGCGGAATCCTCCTGGGAGCTCTGTGGGAGACCGG
 ATGCAACCGAGTACACGCTATTCAGTTCGGGAAGAGCTGGAGAAAAGGCTCTAGGGTGGCGACATCTCCAGGGACCT
 GGGGCTGGAGCCCGGGAGCTCCGGAGCGCGGAGTCCGCATCATCCAGAGGGTAGGAACGCGAGCTTTTGCCTCT
 GAATCCGCGCAGCGCGAGCTTGTGTACCGCGCGGCGAGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTGT
 TCAATTAAATCTAGACATTTGATGGAGGATAAAGTGAAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA
 CGACAATGCGCCTTACTTTCTGTAAGAGTGAATTAGAAATAAAAAATTAGTGAATAATGACGCCACTGAGATCGGTT
 CCCTCTACCCCAACGCTGGGATCCGGATATCGGGAAGAAGCTCTCTGCAGAGCTACGAGCTCAGCCCGAAGCACTCA
 CTTCTCCCTCATCGTGAAAAATGGAGCCGACGGTATGAAGTACCCGGAATTTGGTGTGAAACGCGCCCTGGACCG
 CGAAGAAAAGGCTGCTACCACTGGTCTTACGGCTCCGACGGGGGCGACCCGGTGCACAGGCAACCGCGCG
 CATCCGCGTATGTTTCTGGATGCGAACGACAACGCAACGACGCTTTGCTCAGCCGAGTACCGCGCGAGCGTTCC
 GGAGAATCTGGCTTGGGCAACGAGCTGCTTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATCGGGAAGT
 GAGGTATTTCTCCGGTATGTGAGCGACAAGGGCGGCCAAGTTTTCAAATAGATTGTAAATTCAGGACAAATATC
 AACAATAGGGGAGTTGGACCAACGAGGAGTCAAGATTCTACAGATGGAAAGTGAAGCAATGGATAATGACGAGATA
 TTCTGCGCGAGCCAAAGTCTGTATCACTGTTCTGGAGCTGAACGACAATGCCCCAGAAAGTGGTCTCACTCTCTCT
 CGCCAGCTCGGTTCCCGAAAACCTCCAGAGGGGACATTAATTGCCCTTTAAATGTAAATGACCAAGATTCTGA
 GGAAAAAGGACAGGTGATCTGTTTCAATCCAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAATTTACTA
 TAGTTTAGTACAGACATAGTCTTGGATAGGGAACAGGTTCTAGCTACAACATCACAGTGACCGCCACTGACCG
 GGGAAACCCGCCCTTATCCAGGAAACTCATATCTCGTGAAAGTGGCAGACACCAACGACAAACCGCGGGTCTT
 CCCTCAGGCTCTCTATTCGGCTTATATCCAGAGAACAAATCCAGAGGAGTTCCTCTCGTCTCTGTGACCGCCCA
 CGACCCGACTGTGAAGAGAACGCCAGATCACTTATCCCTGGCTGAGAACACATCCAAAGGGGCAAGCCTATC
 GTCTAGTGTCCATCAACTCCGACACTGGGTAATGATGCGCTGAGCTTCTTGCATACGAGCAGTTCGAGAGA
 CTTGCAAGTGAAGTGTGGCGGGGCAACCGGCCACCGCCCTCCAGCAGCAACGTGTGCTGTAGCCTGTTGCT
 GCTGGAGCAACGACGAATGCGCGCGGAGATCCTGTATCCCGCCTCCCAACGCGGTTCCACTGCGGTGAGTGGC
 GGCTCCCGCTCCGCAAGGCCCGGCTACTCTGTCACCAAGGTGGTGGCGGTGGACAGAGCTCCGGCCAGAACGC
 CTGGCTGTCTACCTGTCTCAAGGCCAGCGAGCGGAGCTCTTCTCGTGGGTCTGACACAGGGCGAGGTGCG
 CACGCGCGAGCCCTGTGACAGAGACGCGCTCAAGCAGAGCTCTGTAGTGGGCTCCAGGACCAACGCGCACCC
 CCTCTCTCCGCACTGTCAAGCTCAACGCTGGCGGTGGCCGACAGCAATCCCAAGCTCTGGCGAGCTCGGAGC
 CTCTGAGTCTCCAGCTATCACTCTGAAACTCAGACCTCACTCTGTACTGGTGGTAGCGGTGCGCGGCTCTGCTG
 GCTCTCTCTGCTCTCTGATCTCTGCTGGCTCAGGCTGCGGCTGGGCAAGTCAAGCTGCTGCTGAGCT
 TTCAAGAGCGGCTTGACAGGAGCGCGCGCTCGCACTTTGTGGGCTGGAGCGGCTGACAGCTTCTCTGACAGC
 ATATTCACAGAGGTTTCCCTCAACAGGACTCGCGAAGAGTCACTGTATCTTCCCGAGCAATATCCCACTTTGGCT
 TGGAGTGCAGCGGTACGATCATAGCTCACTCGGCGCTCAAACTCTAGGCTCAAGCAATATCCCACTTTGGCT
 CGGTGTAAACAGGACTACAGGTGCAAGCCACTACTGTCTGCTATCTATCTATCTATCTATCTATCTATCTAT
 CTATCTATCTATCTATCTATCTTTCTGTACAGAGCGGAGTCTACAGCCTGTAAATCCAGTACTTTGGGAGGC
 CGAGCGCGGTGATCACTCAGAGTTGGGAGTTTGAAGCAGCGCTGACCAACATGAGAGAACCCCGCTTATCTAA
 AAAAAATCAAAATTAGCGCGGCTGTGGTCAATGCTGTAAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAT
 TGCTTAACTCGGAGGTGGAGGTGCAATGAGCTGAGATTGTCCATTGCACTCCAGCTGGGCAACAGAGTGT
 AAACCTATCTCA

FIGURE 157

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLGLILLGTLWETGCTQIRYSVPPELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR
DINDNAPYFRESELEIKISENAATEMRFPPLHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELVLRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLST
ETHISLVNADTNDNPPVFPQASYSAIYPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLVYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVLSLFLVLDQNDN
APEILYPALPTDGGSTGVELAPRSAEPGYLVTKVVAVDRDSGQNAWLRYRLKASEPGLFSVG
LHTGEVRTARALLDRDALQKSLVVAVQDHGQPPLSATVTLTVAVADSIQVLADLGSLESPA
NSETSDLTLYLVVAVAVSCVFLAFVILLALLRLRRWHKSRLQASGGGLTGAPASHFVGVD
GVQAFLQTYSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLSGDSVFSKDSHGL
IEVSLYQIFFLFFNCVSVQAGVQRYDHSSLRPQTFRLLKQLSHLCLRCNRDYRCKPPTVCLS
IYLSIYLSIYLSIYLLLSCTDGSLLTPVIPVLWEAEAGGSPEVGSRLPA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCACAGTTAAAG
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCAATGGGACGCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTCTAGAGTGCCAACCCATTGCGAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCTT
ACAGCTGCCCACTGTAAAAAACCGAAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTCAACAGTCCCGAGAGAATTTTCTGCACTCTCAACT
GTGCAGAAGTAAAAATCTTTC CCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCT
CTGGTTC

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMLLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL
VGGNWLTAAHCKKPKYTTRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGSDDPCGRSDKPGVYTNICRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

FIGURE 160

GGCGCCGGTGACCGGGCGGGCTGAGCGCTCCTGCGGCCCGGCTGCGCGCCCGGGCCCGC
CGCGCCGCCACGCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCGCGCCCGC
GCCCGCGCCAGGTGAGCGCTCCGCGCGCGCGAGGCCCGCCCGCGCCCGCCCGCCCGC
CCCCGGCGGGCGGGGAACCGGGCGGATTCTCGCGCTCAAACCACTTGATCCCATAAAAAC
ATTTCATCTCCCGGGCGCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCCGCGCCCGCCCTCG
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCGAGCCAGCCAGACCCGGGCGGAGC
GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCCGGGCCGTAGCGCGCGCGCTTGGGA
TGGGACCCCGGCCCGGGGAGACGGCGCCCGCCCCGAAACGACTTTCAGTCCCGCAGCGCGC
CCGCCCAACCCCTACGATGAAGAGGGCGTCCGTGGAGGGAGCCGGCTGCTGGCATGGGTG
CTGTGGCTGACGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCTGCGTATGCTACAATGA
GCCCAAGGTGACGACAAGCTGCCCCAGCAGGGCCTGCAAGGCTGTGCCCGCTGGGCATCCCTG
CTGCCAGCCAGCGCATCTTCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCTGCGCAACCTCACCATCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGC
GGCTGCCCTTCACTGGCCTGGCCCTCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
GGTCTGTGGACCTGCCACATTCACGGCCTGGGCCCGCTACACAGCTGCACTGGAGCCGC
TGGCGCCTGCAGGAGCTGGGCCCGGGCTGTTCGCGGCTGGCTGCCCTGCAGTACCTCTA
CTTGCAGGACAACGCGCTGCAGGCACTGCCCTGATGACACCTTCCGCGACCTGGGCAACCTCA
CACACCTCTTCTGCAACGCAACCGCATCTCCAGGTGCCCGAGCGCGCCTTCCGTGGGTG
CACAGCCTCGACCGTCTCTACTGCAACGAAACCGCGTGGCCCATGTGCACCCGCATGCTT
CCGTGACCTTGGCCGCTCATGACACTCTATCTGTTGCCAACAACTATCAGCGCTGCCCA
CTGAGGCCTTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG
TGTGACTGCCCGGCACGCCCACTCTGGGCTGGCTGCAGAACTTCCCGGCTCTCTCTCCGA
GGTGCCCTGCAGCCTCCCGCAACGCTTGGCTGGCCGTGACCTCAAACGCCCTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCATCTGGACCGGCAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCCAAGTGTGCCAGCCAGATGCCGTGACAAGGCCCTCAGT
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGGCCGCCGGTG
ACAGCCCGCCGGCAACGGCTCTGGCCCAACGCGCATCAATGACTCACCTTTGGGACTCTG
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT
CCCCACCTCGGGCCTCGCGGAGGGCCAGGCTGTTACGCAAGAACCGCACCCCGCAGCCACT
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGACTGGTGACTCAGAAGGCTCAGGTGCC
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCTGGCGCTGGTGCTGTGGACAGTGCT
TGGGCCCTGCTGAACCCCAAGCGGACACAAGAGCGTGTCTCAGCAGCCAGGTGTGTACATAC
GGGGTCTCTCTCCACGCGCGCAAGCCAGCCGGGCGCGCCGACCGTGGGGCAGGCCAGGCCAG
GTCTCTCTGATGGACGCTGCCGCCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG
TTCGGCGGCAGCGTTTGTTCAGAACGCCGCTCCACCCAGATCGCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA
AAAA

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184
><subunit 1 of 1, 473 aa, 1 stop
><MW: 50708, pI: 9.28, NX(S/T): 6
MKRASAGGSRLLAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI
FLHGNI RISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDP
TFHGLGRLHTLHLDRCGLQELGPGLFRGLAALQVLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLHQN RVAVHVP HAFRDLGRMLTYL FANNLSALPTEALAP
LRALQYLRLNDNPWVDCRARPLWAWLQKFRGSSSEVP CSLPQRLAGRDLKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAA DKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSGSGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
 TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCAAGCCTCAGATACTGGGGACTTTTAC
 AGTCCCAAGAACCGTCTCTCCAGGAAGCTGAATCCAGCAAGAAACAATGAGGCGCCAGCGGGA
 AGCTCATTGTGACAGAAAGGCAAGTCTCTTTTTCTCTTCTCCTTTGGGCTTATCTCTGGCG
 GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCTAC
 CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTTCCAGGCGGGGGGTTAGGGTTG
 TTTCCAGAGGGAACAAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT
 GAGAAATGAGCCGTGAGGATCTGTGCGGTCAACAGAGCCCTGTGTCTACGTTTCCAAGT
 GTTGCTAGAGAGTCCCTTCGAGTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC
 ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCTCTCTGGG
 ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAAATTAGAGAACTA
 TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACC CGCAACGCGAGTGATGGCAGGAAAT
 ACCCAGAGCTGCTGCTGGACAAAGCGCTGGACCGAGAGGAAGCTGAGCTCAGGTTAACA
 CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCAGCTGCTCAGGTCTACATCGAAGT
 CCTGGATGTCAACGATGCTCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG
 AGGACAGTCCCGTAGGCTTCTCTGGTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC
 AACGGAGAGATTTCTTACTACTTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT
 CAATCCCTTGACATGGAGAAATTGAACATAAAAAACAACTCGATTTCCGAAAACTTCAGTCTCT
 ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAAATGCACCGGTTCTGATT
 CAAGTGTAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCGCCCAAT
 ACCTGAGAACCGCGCTGAAACTGTGGTGTGCACTTTTTCAGTGTTCAGATCTTGATTGAGGAG
 AAAATGGGAAATTAGTTGCTCCATTGAGGAGGATCTACCTTCTCTGAAATCCGCGGAA
 AACTTTTTACACCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT
 CACTACTACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGGTGC
 TGATCGCGGATGTCAATGACAACGCTCCCGCTTCACCAAACTCCTACACCCTGTTTCGTC
 CGCGAGAACCAACAGCCCCGCCCTGCACATCCGACGCTCAGCGCTACAGACAGAGACTCAGG
 CACCAACGCGCCAGGTCACTACTCGCTGCTGCCGCCACGAGACCCGCACTGCCCTCACAT
 CCGTGGTCTCCATCAACGCGGACACCGGCCACTGTTTCGCCCTCAGGTCTCTGGACTACGAG
 GCCCTGCAGGGGTTCCAGTTCCGCGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG
 CGAGGCGCTGGTGC CGTGGTGGTGTCTGGAGCCCAACGACAACTCGCCCTTCGTCTGTACC
 CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCGAGCCGGGCTAC
 CTGGTGACCAAGGTGTGGCGGTGGACGGGACTCGGGCGACAGACGCTGCTGCTGCTGATC
 GCTGCTCAAGGCCACGGAGTCTGGTCTGTTTCGGCGTGTGGGCGCACATGGCGAGGTGCGCA
 CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGTCTGGTCAAGGAC
 AATGGCGAGCCTTCGCGCTCGGCCACCGCCACGCTGCACGCTGCTCTGGTGGACGGCTTCTC
 CCAGCCCTACTCTGCTCTCTCCGGAGGCGGCCCGCCAGGCCACGGCCGACTTGTCTACCG
 TCTACCTGGTGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGTCTCTGTTT
 GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGCGCGCTCGGTGGTGTGCTGCTGGTGGCCGA
 GGGCCCCCTTCAGGCACTCTGTGGACATGAGCGGCACAGGACCTTACCCAGAGCTACC
 AGTATGAGGTGTGCTGCGCAGGAGGCTCAGGACCAATGAGTTCAAGTCTCTGAAGCCGATT
 ATCCCCAATTCCTCCCAAGTCCCTGGGAAAGAAATACAAGGAATTTACCTTCTCCCAA
 TAACTTTGGGTTCAATATTGAGTGAACCATAGTTGACTTTTACATTCCATAGGTATTTTATT
 TGTGGCATTTCCATGCCAATGTTTATTTCGCCCAATTTGTGTGTATGTAATATTGTACGAT
 TTACTCTGATTTTTCTCATGTTCTTCTCCCTTGTGTTTAAAGTGAAACATTACCTTTATT
 CCTGTTCTT

FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQVLFSLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVS RGNKLHLQLNQETADLLNEKLDREDLCGHTPCVLR FQV LLES PF EFFQAE LQV
IDINDHSPVFLDKQMLVKVSESSPPGTT FPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREEAE LRLTLTALDGGSPPRS GTAQVYIEVL DVNDNAPEFEQPFY
RVQISEDSPV GFLVVKVSATD VDTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCSIQEDLPFLKSAENFYTL LTERPLDRESRAEYNITITVTDLGTPLMITQ
LNM TVLIADVNDNAFTAQTSTYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSL LPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGGQFRVGASDHGSPALSSEALVRVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVAVDGDGSGQNAWLSYQLLKATELG LFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAQ
ADLLTVLYLVVALASVSSLF LFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

FIGURE 164

ACCCACGCGTCCGCCCCACGCGTCCGCCCCACGCGTCCGCGCGTAGCCGTGC
GCCGATTGCCTCTCGGCCTGGGCAAATGGTCCCCGGTCCCGGTGCACGACCGCCCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGAATTCCCGTCCGCGGCGTGG
AGGTTCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG
GGGGTGTGTACTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCGAGACAGGGCAGC
AGAAGAGGCCAATCGGCTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG
TGATTCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGCGCTCACCTGTGGTGCT
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTGGATGGCGCTGG
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
GAGAGAAACATTACAGGATTAGAAAAATTCACTCTGAAAAATTTAAATATGTCACAGGACCT
TATGGATTTTCTGAACCCAACCGGTAGTGACTGTACTCTAGTCCGTGTTTACACCCCGTGGT
GCCGCTTTTCTGCCAGTTTGGCCCTCACTTTAACTCTCTGCCCGGGGCATTTCCAGCTCTT
CACTTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACAGGTTTGGCACCGTAGC
TGTTCTTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC
GAACACTGGAAACACTGAAAACTTCACTTTTAAATCAGACAGGTATAGAAGCCAAGAAGAA
GTGGTGGTAACTCAAGCCGACCAAAATAGGCCCTCTCCAGCACTTTGATAAAAAGTGTGGA
CTGGTTGCTTGATTTCCTTATCTTTTAAATTAGTTTTATTATGTATGCTACCATTCGAA
CTGAGAGTATTGCGGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
CATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAAGAATCATTGTGTTGAA
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC
AAAAATATTCAATAG

FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333

><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRRPPRVMLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEEL
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC
NVRESLFLSDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFFPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAQPMARFNHTDRTLETLKIFIFNQTGIEAKKNVVVTQADQ
IGPLPSTLIKSVDWLLVFSLSLFFLISFIMYATIRTESIRWLIPGQEQQEHVE

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296

Thioredoxin domain

amino acids 211-227

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTGCGCGCCCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCTCGCCTCGCACTGCTGCTGGGCTCGGCGCGGGGCTCTTCTCTC
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCTGTGCTCGCTCTTCCCCCGTCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG
CCTTCGGCTTCCCCTGCCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG
ATTTTGCACTGAAAAATAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAATCATC
CTGGAGACCAAGAGCAAGACCATTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCACTGCACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA
GTCCCGGCATCCTGATGGCTCCGACAGGCCTGTCTCCAGAGCACGGCTGACCATTTCTGCTCC
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCTGCCTTTTCACAGTTTGCATCCCCAGCATTTCTCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTTGTAAGAAATATTCAAACCTAATA
AAATCATGAATATTTTAA

FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSARGLFLEGGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETIQPCHSLCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQGELVITSVKRWQKQREFKRISRSIRKLQC

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

FIGURE 168

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGCCGAGACGCGGTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGTGGGTGTTCTGTCTCGCGATC
AGCCTGTCTCACTGTCTCCAAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTATC
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTGCGGCTCCGTGCGGCG
ACCATCCTGGGTGCGTGGCTGAACCTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT
TGTTGGGACCCAAAACCATTTGCCTTCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTTGGTTCACAGAGCACGAGCA
GCCACGGCCAACATGCTCGCCACCATGTGCAACCTCTGGGCGTCCTTGTTGGCCAATGTGCT
GTCCCTGTGTGCTGGTCAAGAAGGGTGAGGACATTCGGTTAATGCTCGGTGTCTATAACCATCC
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCTG
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTTGGATGGGCTCAAGTGCAGCT
CATGTGGAACAAGGCCTATGTGTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCTCGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC
GGCCTCTGTGGCGCTCTCTTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTA
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTGTG
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCCCTTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGCA
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGTCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCTTTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCG
CCTGTGCACCTTCTTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCGGTGGGGCGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCAGCACGGCGACTCCGGA
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGAGCCCCCACCAGCCT
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCGCCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCCGCACATCGA
TGGAGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRITYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLVVSTPFGVAAIWIILDSVGLRAATILGAWLNFAGSVLRMVPVMVGTQN
PFAFLMGQSLCALAQSLVIFSPAKLAALWFPPEHQRATANMLATMSNPLGVLVANVLSVPLV
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQIQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAAATGMIFVLGQAEIGILIMLMTALTVRREPSLSLTCQQGEDPLDWTVSLLMAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWWIT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

FIGURE 170

GTCCACATCTCGTCAACTGGGTCAGGTCCCTCTTAGACCAGCTCTTGTCATCATTTGTGTAAGTGGACCAAC
 TAGCTCCCCAGTAGGGGGTCTCCCTGGCAATTTCTTGATCGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA
 TGCGCTTGCTTTGGGTCCTGCTGTCTTTTCATAACTCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGG
 AAGGACGACCGGGCTGTATCAAGCCATCCAGGAACACTTGAGGACATTTGCCAGCTTTGAAGAATCTTAGTGGTT
 TCTGAATCTAGCCCATTTGGCCCTATGCAATGATGCAACTTCTGCTGGGGCTTTGGGCCAGGTGG
 CTACTTATTTCTTTTAGSGGGATGTGTCAGGAGGTGACCACTCTCACGGTGAATAACCAAGTGTGAGAGAAAGTGGC
 ATCTGTGATCAGTGAATCGGGAAGCTGTGCCAGGAATCGGGCCGGAGGAGAGGCGGAGCGAGCTGGGGCCCTCT
 CCAGGTTGTGTCAGCTCGCTCAGCGCTCCCCATTCAGGTGGACTCTGAGGAAGGCTTGCTCAGCAGCAGGACGGG
 GCTGGATCGAGAGCAGCTGTGCCAGCAGTGGGATCCCTGCGCTGGTTTCTCTTGATGTGCTTGCCACAGGGGATG
 GATCTGTGATGTGGAGATCCAAGTGTGGACATCAATGACACCGACCGCTGGTTTCCCAAAGGCGCAGGAGGA
 GCTGGAAATCTCTGAGAGCGCTCTCTGCGAACC CGGATCCCCCTGGACAGAGCTCTTGACCCAGACAGCGGCC
 TAACACCTCGCACACCTACACTCTGTCTCCAGTGAGCACTTTGCTTGGATGTCAATGTGGGCCCTGATGAGAC
 CAAACATGCGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCAATTTTGTATCTGGTGTAACTGC
 CTATGACAATGGGAACCCCCCAAGTCAGGTACAGCTTGGTCAAGTCAACGCTCTGGACTCCAATGACAATAG
 CCGTGGCTTTGCTGAGAGTTCACTGGCCTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAATCT
 GACCGCCACAGACCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCTCCCAAGAGT
 GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCACTTCTGCGTGCACCTTAGACTATGAAAGAACCC
 TGCTCTCAGAGTGGAGTGTTCAGGCAAGGAGCTGGTCCCAATCCATCCAGCCCATCTGAAAAGTTCTCATCAA
 GTCTTCTGATGTCTCAATGACAACTCCCAAGCATCCACGTACACATGGGCTCCAGCCATCACTGGTGTGAGAAGC
 TCTTCCCAAGGACAGTTTATATGCTCTTGTCATGGCAGATGACTTGGATTGAGGACAAATGGTTTGGTCCAATG
 CTGGCTGAGCCAGAGCTGGGCCACTTCAGGCTGAAGAAGAACTAATGGCAACACATATGTTGCTAAACCAATGC
 CACACTGGACAGAGAGCAGTGGCCCCAATAATACCTCACTCTGTGTAGCCCAAGACCAAGGACTCAGCGCTTATC
 AGCCAAGAAACAGCTCAGCATTCAGATCAGTGACATCAACGACCAATGCACCTGTGTTGAGAAAAGCAGGTATGA
 AGCTTCAAGGCGAAAAACCACTTACCTCTCTTCACTCATTACCTCAGGACTCAGATGACAGATGCGAGCTGGCAGT
 TAATGAGAGTCTCTATACCGCATCCAGGACTCCCGAGTTGCTCACTTAGTAGCTATGATCTGCAACACAGGAGA
 GCTCACTGTCTCAGAGTGTCACTGAACATGAAGAGATGGCGGCTTTGAGTTTCTCAGGTGATCCGACAGGACGCG
 GCAACCCATGTCTGATCCAGTGTCTCTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCACAGGTTGGTGT
 CCAGCTGTCTGCTCAGCGATGAGGAAACAGGACCTCTCCGTGCTGTGAACTGTCAGGCTCTCAGCGGCTGCTGTGTG
 CATCGACATCCCAATGGCTGGGCCAGCGGGCACTGACACACTCCACTGCCCCTCAGCATCCCGGCCCAT
 CTTTTGACCAACTTGTGGCAGAGATGCAGACTCGGGGCCAATGGAGAGCCCTCTACAGACTCCCAATGG
 AATGAGGCCACTCTTCACTCTCAACCTCATACGGGGCAGCTGTTCGTCATGTCACCAATGCCACAGCCT
 CATTGGGAGCTGTGGAGCTGGAGATAGTAGAGACAGGGAAGCCCCCTTACAGACTCAGGCTGT
 GAGGCTCATGTTTGTCCAGAGTGTGACCACTGAGGACCTCAGCCCGCAAGCCTGGGGCTTGAACATCTGCTGAT
 GCTCAGCTGATCTGCTCGCTGTGATGTTGGGCATCTCGGCTGATCTGGCTTTGTCATGCTGCTCGCG
 GACAGAAAAGAAGGACACAGGGCCCTCAACTGTGCGGAGGCGAGTCCACTTACCGCCAGGACCCAGAGAGCC
 CCAGAAACACTTCCAGAAAGCGAGACATCCACTCTGTGCTGTGCTCAGGGGTCAAGGCTGAGCCTGTGAAAT
 CGGCGAGTCCCAAGAGATGTGAGGAGGCGGATGATGGAAGCAGGCTGGACCTGCTGCTGAGGCCCTT
 CCACCTCACCCCGACCTGTACAGGACGCTGCGTAAATCAAGGCCAACCAAGGACAGCCGGCGGAGAGCCCGAGAGT
 GCTGCAAGACACGCTGCAACCTCTTTTCAACACTCCAGGCAGAGGAATGCTCCCGGGAGAACCTTGAACCTTCC
 CGAGCCCGAGCTGCCACAGGCCAGCCAGCTTCCAGGCCCTCTGAAGGTTGCGAGGACCCCAAGGAGGCTGGC
 TGGAGACAGGGCAGTGAGGAAGCCCAAGAGGCCCAACAGCCTCTCTGCACTCTGAGACGCGACGACATCT
 CAATGGCAAGGTGTCCCTGAGGAAGAAATCAGGGCCCGCTCAGATCTCGGGAGCTGTGCTCGGCTGTCTGTGG
 TGCTCTCGGAGCGGAACCCGCTGGAGGAGCTCACTGTGAAATCTTCTCTCTGCTGCTGCAATCTCCAGCTGTCT
 GTCTTCTGTGATCAGGGCCAAATTCAGGCCCAACCAACCAAGGAGGAATAGATCTTGGCCACAGCCAGGAGG
 GACGAGGATGTCATCCAGACAGATGGCCCAAGTGCAAGGCTGGAGCCAGACAGACAGCAAGGAGGA
 AGGGCTCTTGGATCTTGAAGAGGACCTCTCTGTAAGCACTGTAGAAGAGAGCTGTCAAGTGTCTGTGAGAAC
 CAGCACAGTCTGCCCCCTGAGCCCGCTGAGCGCCCTCAGCCCGGCTGGATGGCAGACTCTTTTGCCCCCTCAC
 CACCAACTACCGTGACAAATGTGATCTCCCGGATGCTGCAGCCACGAGGAGGAGCCAGGACCTTCCAGAGCTTCGG
 CAAGGCAGAGCCACAGAGCTGATGCCCAACAGGCACAGGCTGGCCAGCCTTGGTCTCGGAGTGGAGCTCACT
 GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCCGTTGGAGGCGCGCTCGAGGCGCTCGCGCGGCTCTCGT
 CTGCGGGAGGACCTCTAGTTTAGACTTGGCCACAGTGCAGCTCAGGCATGAAATGCAAGGGGACCCAGGTGG
 AAGAGCGGGAATCAGGGCCAGAGCAGAGGACAGCAGCAGCAGCAGCAGGTCCTGTGAACATACCTCAGACGCTC
 CTGATCTCAAGAAGCAAGGGCTCTGAGGATCTGTGGACAAGAGCTGGTTCTAAATCTTGTAACTCACTAGCTAG
 CGCGGCGCTGAGAATTTAGGTGATGATGATCCCCACAGAGAGGCGCAAGGCCCGGACCTAACAGCTGAC
 GTACCAAGCAGGCCCTTGTGAAGCAGCTCTGAGTCTTTTGGAGGACAGGACGCGTTGTGGCTGAGATAGTGTT
 TCTCTGCAAAACATATGTGGACCAAGGGTCAGTCTCTCGGCAGAACAGATGCCAGGAGTATCAGGCGAG
 AAGGGTGGCTCTTTGGGTAGCAGGAGTCAGGGGGCTGTACCTTGGGGTGGCAGGAATGCTCTCTGACCTAT
 CAATAAGGAAAAGCAGTAAAAA

FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331
<subunit 1 of 1, 1184 aa, 1 stop
<MW: 129022, pI: 5.20, NX(S/T): 5
MMQLLQLLGLLGPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLPQALPIQVDSEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQ
VLDINDHQPRFPKGEQELEISASLRTRIPLDRALDPDTPGNTLHTYTLSPSEHFALDVIV
GPDETKHAEILIVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNSPAPFAESS
LALIEQEDAAPGTLTKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGNPIPAHCKVLIKVLVDNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHADLGLINGKVS
YRIQDSPVAHLVAIDSNTEGVTQAQRSLNVEEMAGFEQVIAEDSGQPMLASSVSVVWSLLDA
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTTPPLATHSSRPFLLT
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQPKRPQKHQKAD IHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA
GWDPCQLQAPFHLTPTLYRTLNRQGNQGAPAESREVLDQTVNLLFNHPRQRNASRENLNLP
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEPQRPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGQFQPKPNHRGNKYLAKEGGS
RSAIPDTPGSPARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNRYRDNVISPDAAATEEPRTFTQTFGKAEAPELSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDSLATSASGMKVQGDPGGKTGTGKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGAGAGCCGCAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTGGATTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCAACAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAATGAACCTGTGTGAATTCTGCTGATCCTGGTTTTCATGGTGCCTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACACGACTGCTTTTTCCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGAACTAGGAGATCCCTTTCCATTCTCAGCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGACTCTC
ATGGCTCTTCTTCTGGAATTGGTGTGTCAACTGCCATACACTTACATGTCTTACTTCCT
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCAGGAGAACAATGTTCCAGAAGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTACCATTCTCAGCATCAGG
AAGTGAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAACAGCTGATCTATATGCTACCAAGGAGAGAAATAGAACTCCAAAACCTTC
AAGGGGAAATATTTAAATTTCTTGGTTACTTTTCTCTATTACTGTGTTTGAAAAATTTT
CATGGCTACCATCAATATTGTTTTGATCGAGTTGGGAAACGGATCCTGTCAAGAGGCCA
TTGAGATCACTGTGAATTATCTGGAATCCAATTGATGTGAAGTTTGGTCCCAACACATT
TCCTTCATTCTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCATTGTCTGCTATTAGCAC
AGATAATGGGCATGTACTTGTCTCCTCTGTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCATAATCACTGAAGTCTTGGAGAACTGCAGTTCAACTTCTATCACCCTTGGTT
TGATGTGATCTTCTGGTCAGCGCTCTCTAGCATACTCTTCTTATTGGCTCACAAAC
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAAACGAGGCGTGACATTTATAAAC
AAACAAATGCTATGGTAGCATTTTTCACCTTCATAGCATACTCCTTCCCGTCAGGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGCCAAGAACTAA
AGGTGAAAAATACTGGAACTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT
AGGATTTCCGTTTAAAGTTTCACATGGAAAAGGTTATAGCTTTGCTTGAAGTTGACTCATT
AAAATCAGAGACTGTAACAAAAAAGGGCGGCGGCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTATTGACAGTTATAATG

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYPFHWMNLCVILLILVFMVPPYIGYFIVSNIRLLHKQRLFLSCLLWLTFFMYFF
WKLGDPPILSPKHGILSIEQLISRVGVIQVITLMALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALEELSRLQFLETADLYATKERIEYSKTFKGKYFNFGLGYFFSIYCVWKIFMATINIVF
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCGANACTATTTTTTGGATTGGGGTGGCTTTTCCTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCAACATGTTTGAGCTCATCATCTTTGAAATCTNNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATCCGGGTNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGT CAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCAACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCGCTGATC
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTCCTC

FIGURE 176

CTCGCGCAGGGATCGTCCC**AT**GGCCGGGGCTCGGAGCGCGACCTTGGGGGGCCCTCGGGATTGTCTACCTTTT
TGGCTCCCTGCTCGTGAACCTCTCTTCTCA CGGGCTGTGCGCTTCAATCTGGA CGTGTATGGGTGCTTCGCGCAA
GGAGGGCGAGCCAGGCGCTCTCGGCTTCTCTGTGGCCCTGCACCGGCAAGTTGACGCGCGACCCCGAGAGCTG
GCTCGTGGTGGGTGCTCCCGAGGCCCTGGCTCTTCTCTGGGCAGCAGCGGATCGCATCGAGGCGCTCTCGCTTG
CCGCTGTAGAGCGACCGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACTGGCACACCTGGACAGCGG
GGAGAACCAAGTGGTGGAGTCACTGTCTGGAGCCAGGGCTCGGGGCAAGATTGTATCTGTGCAACACCGATA
TGGGGCAAGGCGAGCTGGACCCAGATCTTGGAGACGCGGGATATGATTGCTGCTGCTTGTGCTCAGCCAGGA
CTCGGCCATCTCGGGATGAGTGGATGGTGGGGAATGGAGTTCTGTGAGGGGACGCCCCCAAGGCCATGAACAAAT
TGGGTTCTCGCAGCAGGGGCAAGCTGCGCGCTCTCTCCCTGTATAGCACTACCTCTCTTTTGGGGCCCGCAGAAC
CTATAATTGGAAAGGGCACCGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACTGGCACACCTGGACAGCGG
TCCCTACGAGGCGGGGGGAGAGGAAGGAGCAGGACCCCGCTCATCCCGGTCTCTGCCAACAGCTACTTTTGGCTT
CTCTATTGACTCGGGGAAAGGCTGTGGTGCCTGCGAAGAGCTGAGCTTTTGGCTGGAGCCCCCGCGCCAAACCA
CAAGGGTGTCTGGTTCATCTGCGCAAGGACAGCGCCAGTCCGCTGTGTGCCCGAGGTTATGCTGTCTGGGAGCG
CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTATGGCTGGCCAGACCTGATAGTGGG
TGCCCTCACTCTTTTGGAGCGCAAGAAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACAGGGGGGTCACTG
GGCTGGGATCTCCCTCTCGGCTCTCGGCTCCCTGACTCCATTTCCGGATCAGCGCTGGCTGTCTCTGGGGGA
CTCTCAACCAAGTGGCTTCCAGATAATGTAGTGGGTGCCCTTTGATGGTGTATGGGAAAGTCTTCACTATCCA
TGGGAGCAGCCTGGGGTTGTGCGCAACCTTACAGGTGCTGGAGGGCGAGGCTGTGGGCTCAAGAGCTTCCG
CTACTCCCTGTGAGGCGAGCTTGGATATGGATGGGAACCAATCCCTGACCTGTGTGTGGCTCCCTGGCTGACAC
CGAGTGTCTCTTCAAGGGCGAGACCCATCTCCATGTCTCCATGAGGTTCTATTTGCTCCAGAGCATCGACCT
GGAGCAGCCCAACTGTGTCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCACTACATTTGAGTCCC
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTAGATGCGGACAGACCGGAGGCTCGGGGCCAGGT
TCCCGGTGTGACGTTCTGTAGCCGTAACTTGAAGAACCCAAAGCACAGGCTCGGGCACCGTGTGGCTGAAGCA
CCAGCATGACCCGAGTCTGTGGAGAGCCCATGTTCCAGCTCAGGAAATGTCAAAGACAACTTGGGCCAATTGT
AGTGACCTTGTCTTCAAGTCTCAGACCTCCGCTCCGGCGACAGGCTCTGTGGCAGGGGCTGCCTCCAGTGGC
CCCCCTCTCAATGCCACCAGCCAGCACCCAGCGGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGCA
CAAGATCTGCCAGAGCATCTGCAGCTGTGCTCAAGCCCGCTTCTGTACCCGGGTGAGCGACAGGAATCTCAAC
TCTGCCCATGTGATGGATGGAAACACAGCCCTGTGTTGCACTGAGTGGGCGACAGCTCATTTGGCTGGAGCTGAT
GGTCAACCAACTGCCATCGGACCGACCCAGCCCGAGGCTGATGGGGATGATGCCCATGAAGCCAGCTCTGTGT
CATGCTCTCTGACTCATCTGCACTACTCAGGGGTCCGGCCCTGGACCTGCGGGAAGAAGCATCTGCTGTCCAA
TGAGATGTGCTCCATGTGAGTGTGAGCTGGGGAACCCCATGAAGAGGGGTGCGCCAGTCACTCTTACCTCAT
CTTACGACCTCCGGATCAGCATGTGAGACACAGGAATGGAGGTAGAGCTGTGTTGGCCACGATCAGTGAAGCA
GGAGCTGCATCTCAGTCTCTGACAGAGCCGCTGTCTTCAATTGAGCTGCCACTGTCTCAATTCAGGAAATGGCCATCC
CCAGCAACTCTTCTCTCTGGTGTGGTGAAGGGCGAGAGAGCATCAGCTGTAGCGGGATGGGGCGAGGCTCGG
CAGTATGAGGTCAAGCTTCCAAACCAAGCCAGTCCGCTCAGAACCTTGGCTCTGACCTTCTCAACATCATGTG
GCTCATATGAGTTGCAATGGGAATGGTGGCTGTATGCCAATGCAAGTTGAGCTGAGGGCGGGCGAGGGCCGTG
GCAGAAAGGGCTTTGCTCTCGAGGCCCAACATCTCCACTGGATGTGGACAGTAGGGATAGGAGGCGCGGGGA
GCTGGAGCCACTGAGCAGCAGGAGGCTGTGTGAGCGGGCAGGAGCCCGACGATGTCTGTGTGGCCAGTCTCTG
TGAGAAGAAGAAAAAATCACTCCCTGACTGCGCCCGGGGCGACGGCCAACTGTGTGGTGTTCAGCTGCCACTCTA
CAGCTTTGACCGCGGGCTGTGCTGATGTCTGCGGCCGTCTCTGGAAACAGCACTTTCTGGAGGGATCTCAGC
TGTGAAGTCCCTGGAAGTGATTGTTCCGGGCAACATCAGTAGTAATCTCCATAAAGAACTTGATGCTCCGAGA
TGCCTCCAAGTGTATCCAGTGTGATGGTATATCTTGAACCCATGGCTGTGGTGGCAAGAGGATGCCCTGTGGGT
CATCTCTTGGCTGTATCTGCTGGGGCTGTGGTGTATGACACTGCTGTGCTGTCTGTGGAGATGGGATTTCTT
CAAAAGGGGCAAGCACCCCGAGGCCACCGTGCAGCCAGTACCATGTGCGGTGAAGATTCTCGGGAAGACCGACAGCA
GTTCAAGAGGAGAGAGACGGGACCCATCTTGAAGGAACAATCGGGGCGACCCCGGGGAGGGGCCGGATGCACA
CCCCATCTGGCTGCTGA CGGGCATCCGAGCTGGGCCCGATGGGCACTCAGGGCCAGCAACCGCT**AG**GTTC
CATGTCCAGCTGGGCTGTGCTGCCCTCCATCCCTCCAGAGATGGCTCTGGATGGAGTGGGATGGGTAGAT
GGGCTGTGCTGTGCTGCAATCAAGATTGGCAGGATCGGCTCTCTCAGGGGCAAGACCTCTCCACCCACAGAAC
TCTCTCCACCAACTCTCCCTTAGATGTGTGAGATGAGATGAGATGAGGTAATCAGGAGCAGGCGCATGGGGTAGGG
TGAGAAAGGGCAGGGGTGTCTGATGCAAAAGGTGGGGAGAAGGGATCTTAATCCCTCTCTCTCCATTCACCTGT
GTAACAGGACCCCAAGACCTGCGCTCCCGGAAGTGCCTTAACTAGAGGGTGGGGAGGAGGTGTGTGCTCACTGA
CTCAGGCTGCTCTTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTGCGCATCAGTCTAGTGGTTCGTGGT
TTGCTCTATTATTAATAAATATTGGAGAACAAAAAATAAAAAA

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGAAGGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPOALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGGGKIVTCAHRYEARQVRDQILETRDMIGRCFVLSQDLAIRDELDDGGEWKFCBG
RPQGEHQFGFCQOGTAAAFSPDSDHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSGFGYSLAVADLNSDGDWPDLLVGA PYFFERQEBELGGAVVYVLYNQGGHWAGI
SPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAGAPFDGDGKVFIYHGSSLSGVVAKPSQVLE
GEAVGIKSPFGYSLSGSLDMDGNQYPDLLVGS LADTAVLFRAPRILHVSHEVS IAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSYLQTPRLRRQAPGGQLPPVAP
TLNAHQPSQTRAEIHLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN
ENASHVECELGNPMKRAQVTFYILISTSGIS IETTELEVELLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVTVSNQQQSLRTLGS AFLNIM
WPHEIANGKWLlyPMQVELEGGQGPQKGLCS PRPNILHLVDVSRDRRRRLEBPPEQEPGE
RQEPMSWNPVSSAEKKNIITLDCARGTANC VVFSCLPLYSFDRAAVLHVWGRLLWNSTFLEEY
SAVKSLEIVRANITVVKSSIKNLMLRDASTVIPVMVYLDPMAVVAEGVPMWVILLAVLAGLL
VLALLVLLLWKMGFFKRAKHPEATVPQYH AVKIPREDRQQFKEEKTGTILRNNWGS PRREGP
DAHPLIADGHPGLGPDGHPGPGTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGTGGCT
CACACAAGATGTGCTCAAGGTGTAGCCGTAAGTGTGTGTGTGCAGCCGCTTGGTGAGTCA
GTCTCTCGCAGCTGCCGCGGGCGGTGGCTGCAGCCGGGGGCGGTGCGAGCGCGGTAATTTTC
TGGATGATAAACAAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCATTGGAGTCCAGGAAAAACCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCCTTCAGATAAGCCCAAGTACAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCAGGGAAGTGGCAAAACAGATTGCGGGACTGGTTCAGAGCCCTTCATGAAAGTGGAA
GTCAAAAACAAGAACAAAAACATTGCTGAGGCTCGAGAGAAGCAGATTGATACCAAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAACTATGACCT
GCTATTGGACCACTCAGAGCTCAGAAGCATTTACCTTGATAAGAAATGAACAGTGTACCAAGG
CATTCTTCAATCTTGTGACACATACAAGGACAGTTTAAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAGGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGT CATGGCAGTGTGGACAGTGCTGGTGTGTGACAGATATGGAATGAAGTC
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGAGAGATT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTATGAC
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAAATTATCTTCTCCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTGTATAATTATTTGAAAAATTCAGCTAAAGTTATAGAACCTTATGTTTAAAT
AAGAATCATTGTCTTGAAGTTTATATTCCTTACACAAAAAGAAAAATACATATGCAGTCTA
GTCAGACAAAATAAAGTTTGAAGTGCTACTATAATAAATTTTTCACGAGAACAACTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAAG
ATAATCTAAGTGAAATTTAAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCATGACTCCAAAAAAAAAAAAAAAA

FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAWCSQSLAAAAVAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKFPDQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKTKTLRPERSRFDTSILFI
CKDSLGMFMFNRLDTNYDLLDQSELRSIYLDKNEQCTKAFNNSCDTYKDSLISNNEWCYCFQ
RQQDPQCQTELSNIQKRQGVKLLGQYIPLCDEDEGYKPTQCHGSVGGQWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

FIGURE 180

CAGACTCCAGATTTCCTCTCAACCAGGAGGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC
 CTCCTTTACGCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGCTGCCCTTCCCGTGTCTCTTCTGGCC
 GCTCTGCCCTCCGCTGCTGCTCGCTGGGGCGCGGCTTCACACCTTCCTCTGATAGCGACTTCACCTTTACCTCT
 CCGCGCCGCCAGAGAGAGTGCTCTTACCAGCCCATGCCCCGAGAGCCCTCGCTGGAGATCGAGTACCAGTGTTTA
 GATGGAGCAGGATTAGATATTGATTTTCCATCTTGCCTCTCCAGAAAGCAAACCTTAGTGTTTTGAACAAAAGAAA
 TCGATGAGAGTTCACATCTGTAGAGCTGAAGTTGGTGATTACATGTCTTCTCTTTGACAAATACATTACGACCCATT
 TCTGAGAAGGTGATTTTCTTTGAATTAATCTCGATATAATATGGGAGAACCGGCAACAGAAAGAGTTGGAAG
 AAATATATTACTGGCAGCATATATTGGATATGAAACTGGAAGACATCTCTGGAATCCATCAACAGCATCAAGTCC
 AGACTAAGCAAAAGTGGGCACATACAAATTTGTCTTAGAGCATTTGAAGCTCTGTATCGAAACATCAAGAAGAC
 AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAAATTTAGTGGTCTATGGTGGTGTGTCAGCCATTCAGATTTTAT
 ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAAACTCCAACTAGAGTACGTAAACATTGAAA
 AATGAGGCATAAAAATGCAATAAACTGTTACAGTCAAGACCATTAATGGTCTTCTCCAAAATATTTTGAGATATA
 AAAGTAGGAAACAGGTATATAATTTAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGATTAATCCTGCTGATCCAG
 TTGTACTTAAGTGTGTAAACAGGAATATTTTGCAGAAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCAT
 TTTCTTAACTTTGAAAAATTTTGCAAAATGCTTGTAGTGATTTAAATAAATGAGTATGGGCCAATTTGCAACACC
 AGTCTGTTTTTAAACAGGTCTATTATCCCGAACTTTTGTGAAATGCGGCAGTTACAAATTAACGTGGAAAGTTT
 TCGATTTTAAAGTTATAAACTACCTGAGAAATACCTAATGATGGAATGAATAAATCTTTAGACTACAAAAGCCCAA
 CTTTCTCTATTATTAATATGCAATCTCTCTATAATGTAAATAGAATATAGCTTTGAAATCAAAATTTGAGATATA
 AGATTTTATGACCAATACATTTCAAGTGTAAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC
 CCAAAAGCTACATTTTCAAGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGCATGTTTTCTCTTTG
 AAATGAAGAAATATAGTTTAAAGAGCTTCTCTCCATAGGACACATTTTCTTAAACCCTTAACATAAGTGTAGGA
 TTTTAAAAATTAATGTGAGGTAAAAATAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
 TAATCATGTTATGTTAATTTTAAACATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATA
 TTGCTAAATGATCTGGGCCATACCATAAATAAATATCTCTTTCTGAGCTCTAAGAATTATCAGAAAAACAGGAA
 AGAATTTAGAAAACTCTGAGAAAACCTAATCCAAAATAAAATTTCACTTAAGTAGAATATAAATAAATCTAGA
 ATCTGACGTGCTCACTGTGACATCCCTACTACATAACATAAAATCAAAGGAGATGTTAATTTCCAGTTAGCTGGAAG
 AAATCTTGGCTGTAGTGTTTTATTTTCTACAAGAATCTGGTTTGAATTTTGTGAAGCAGGTACATTTTATA
 AAATGTAGCCCTACGTGTAAAGTTTACACTGGGTGACATTTTATTAATAAATTTTATTAACAACTCTTTAT
 TAAAAATGGCCTTTCTGAACACTTTATTTATTGATGCTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTAAAC
 CACCTAAATGTGAATAAACCCATTTATCATGATGAATGAACATAAATTTTAAAGTTATGCCCCATTATACGTTGTTAT
 TCAAGTACTAGTAATTTAACTTATCATGATGAATGAACATAAATTTTAAAGTTATGCCCCATTATACGTTGTTAT
 GACTACATTTGTAGTTAGAAAACAAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAAT
 CTTGATGAGCAATAATGATAACCCAGAGAGTGATTTCAATTTACACTCATAGTAGTATAAAAAGAGTACATTTCCC
 TCTTAGGCCCTCGGAGAGAGAGCAGCTTAGATTTCCCTACTGGCAGGTTTAAAAATGAGGTAAGTAAATCCGCTAT
 ATGATCAATTACCTTAAATTTGGCCAGGAAATGCTTCAGGTGTCTAGGGGTATCTCTGCAACATCTGCAGAACAA
 AGGTCAATAAGATCCTTGCCTATGAATACCCCTCCCTTTTGGCTGTGTTAAATTTGCAATGAGGAGCAAAATTTACA
 GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGTCATCTTTCTATAAACTGTGATTAAGCAATCTTA
 CCTCTCCTGTATGGCTGTACTGTACTGTACTCTGACTCCTTACCTTAACAATGAATTTGTTACATAATCTCTT
 ACATGTATGATTTTGGCCATGATCTTAAACCTATGATTCAGTAACCTTTACCATATAAAAAACGATAATTGCTT
 TATTTGGAAGAAATTTTAGGAATACTAAGGACAAATTTATTTTATAGACAAGTAAAAAGACAGATATTTAAGAG
 CATAAACCAAAAAGCAAAACTTTGAAAAACAGAGTAAAAATCTTAATATTTCTAAAGACATAGCTTTTATCTGCT
 CATAGCTCTTTTAAATTTTCACTATTCATTTCTAAATTTAAAGTTATGCTAAATTTAGTAAAGCTGTTTATCACTT
 CAACAGCTCATTTTGTCTTTTCCAATATACAAATTTTAAAAATACTACAATTAATTTATGGTAAAAATTAATCCTTTA
 CATATGTAGAGCATTTACCGTGTTCACCTCACACTAAGGCCATAGAGTTTGTCTGATATGCAATTTGGATGCTTAAT
 GTTATGCTGTTCTTTCTCATGTAGTGTCAAGACATGGAGGTTTGTGTAATTTATGGTAAAAATTAATCCTTTA
 CACATAATGGTGTCTTAAAAATGACAAAAAATGAGCATCTACAATTTGATGTCTCTCAATGAAGATCTTTTAT
 GTGAAATTTTAAAAAGCAATTGATTCGCGATGTAAAGGATTTTTCATCTGAAGTACAATAATGCACAAATCAGTGTG
 CTCAAACTGCTTTATACTTATAAACAGCCATCTTAAATAAGCAAGTATTGTGAGTACTGATATGATATATAATAA
 AAATTTATCAAGGAAAA

FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPFPVLLAALPPVLLPGAAGFTPSLDSDFTTLPAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFTEL
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRKRSRT

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTCGCAGACACTATGCTGCCCTCCCATGGCCCTGCCAGTGTGTCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACGGC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTCAACAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCATATGTCTGCAAGTTCAAGGACTAGGGCGAGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTATGATCCTCC
TTCTTTTTCCTTTTCTTCACCTTCATTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLSGAEGSFVSSILVRSISNSYSYIWIWGLHDPTQGSEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

FIGURE 184

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCAATGCGGGGGACGCGCTGGCGCTCCTGGCGCTGGTGCTGGC
TGCTTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGCTGCAATACTG
AGCTGTGCAATGTAGACGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP
FQGDSTVTKSCASKCKPSDVDGIGQTLFVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCTGACTCTGCAGCCGAACCGGC
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGATGG
TAGCGGCGGCTCTCGGCGGCACCCCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC
AATTCCAACGCTATCAAGAACTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGC GGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACG CAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCAGAAGAACCACCTTGTCTTCAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAACCTGTCTCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGA CTAGAAATATTCAGCGTTGTTACTGTGGAGAAGGCTCTGTC
TTGCCG GATACAGAAAGATCACCATCAAGCCAGTAATTTCTTAGGCTTCACACTTGTGAGA
GACACTAAAC CAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAAC TCCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATCTCAGTGTGGCACTTACCTGTAATGCAATGA
AACTTTTAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTCTCTTGTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATCTATATTGAAC TGAAGTAAATCAT
TCAGCTTATAGTTCTTAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAATGTAACTGAAAACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTTATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAA AAAAAA

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQOTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRKRRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGVCTKHRRKGSHGLEIFQRCYCGEGLSRIQ
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTCTTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGCGGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

FIGURE 189

GAGGAACCTACCGGTACCGCGCGCGCTGCTAGTCCGCGGTGTGGCTGCACCTCACCAATCCCGTGGCGCGCGG
 CTGGGCGCTCGAGAGTGGCTGTGCTTCTCTCTGTCAGCGGTGCTTGGGCTGGCGCAGGCGGGGTGCGCGCGCA
 GGGTTTGAGGATGGGGAGTAGCTACAGGAAGCGACCCCGGATGGCAAGGTATATTTTGTGGAATGAAAGGGA
 AGTATTAGAAATGAGCTGAAGACCATTCACAGATTAAATTTTGGGACAGATTGTGATGTCTGATTACCTCT
 TGAAGTATGTAGACAGAGTTCTCAAAATTTGCATATACATCAACTGGAAACAGCAGTAGATCTTAATGTTCAC
 TTAATCAGAACCTTGCAATAAGGAAGAGATGGGAGTCTGGTTAAATAAAGTAGCTATATACAGAGACTTGAAGAG
 GATCATCTCTGTTTTCGTAGTGTATATGGGCCATTTTGTGGGCAGAGTACAGGATTTTACAGTTTACTTGG
 AGTGTCCAAATCGCAAGCAGTAGAGAAATAAGACAAGCTTCAAGAAATTTGGCATTTGAAGTTACATCTGAGATAA
 AAACCCGAATAACCAAAATGCATAGCGGATTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGTAGAAGA
 TCTACCGAAATAGTATGACAAATGTGGAGAAAGGGACTTGGAGTAAATCAAGTGGCCAGTATGAAGCTGGAA
 CTATTATCGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATAACTTTGAAAGAGAAGAAATTTGATCC
 TGCTGTAAATCTGGAGAACTGTGGTTTGTAAATTTTACTCCCGAGGCTGTTTACACTGCGCATGATTTAGCTCC
 CACATGGAGAGACTTTGCTAAAGAAAGTGGATGGGTACTTGAATTTGGAGCTGTAACTGTGGTGATGATAGAAT
 GCTTTGGCGAATGAAAGAGTCAACAGCTATCCAGTCTCTTCAATTTTTCGGTCTGGAATGGCCCCAGTGAATA
 TCATGGAGACAGATCAAAAGGAGAGTTTGTAGTGGTTTTCGCAATGCAGCATGTTAGAAATACAGTGACAGAACTTTG
 GACAGGAAATTTTGTCAACTCCATCAAACTGCTTTTGTCTGTGTTTGTGGCTGGCTGATCACTTTTGTTCAAA
 AGGAGGAGATTTTGTACTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCAACTATGTTGGATCTCAA
 AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAACACTCTTCGGCAACACACATAGAGGATCGTTT
 GGCTCATCATCGTGGCTGTGTTATTTTTCATTTTGGAAAAAATGAAATTCBAAATGATCCTGAGCTGAAAAAATC
 AAAAATCTTCACTTAAAGATGATCATATTCAGTTTGGCAGGTTTGTACTGTTCTCTGACACAGACATCTGTAGTAA
 TCTGTATGTTTTCAGCGCTCTCTAGCAGTATTTAAAGGACAAGGAACCAAGAAATGAAATTCATCATGGAAA
 GAAGATTCTTATGTATATCTTGTCTCTTGGCCAAAGAAAGTGTGAATTTCTCATGTTACACGCTTGGACCTCAAAA
 TTTTCTGCCAATGACAAAGAAAGTACCTGGCTGTGTTATTTCTTGGCCCCCTGGTGTCCACAGTGTGAGCTTTACT
 ACCAGATTTACGAAGAGCATCAAACTCTTCTTATGGTCAGCTTAAAGTTTGGTACAGTATGTACAGTTTATGA
 GGCATCTGTAAATCATGTATAACATTCAGGCTTATCCAAACACAGTGGTATTCAACAGTCCAACTTCATGAGTA
 TGAAGGACATCACTCTGCTGAACAAAATCTTGGAGTTTATAGAGGATCTTATGAATCCTTCAGGCTTCCCTTAC
 ACCCACCCTTCAACGAATAGTTTACACAAAGAAAACACACAGGAGTCTGGATGGTGTGATTTCTATCTCCGTG
 GTGTATCTTCACTCAAGTCTTAATGCCAGAAATGGAAAAGAAATGGCCCCGACATTAATCTGAGATGATCAACGTGGG
 CAGTATAGATTGCCAACAGTATCACTTTTGTGCCCAGGAAAACGTTCAAGATACCTCGAGATAAGATTTT
 TCCCCAAAATCAAAATAAGCTTATCAGTATCACAGTTACAAATGGTTGAATAGGATGCTTTATCCCTGAGAAT
 CTGGGCTTAGGATTTTACCTCAAGTATCCACAGATCTAACACCTCAGACATTCAGTGAAGAAATTTCAAGG
 GAAAAATCATTGGGTGATGATTTCTATGCTCTTGGTGTGGACCTTGCACAGAAATTTGCTCCAGAAATTTGAGCT
 CTGGCTAGGATGATTAAGGAAAAGTGAAGAGCTGGAAAAGTAGACTGTACAGGCTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAGGCGCTATCCAACTGTAAAGTTTATTTCTACGAAAGAGCAAGAGAAATTTCAAGAAAGACGA
 GATAAATACAGAGATGTCAAAGCAATCGCTGCCCTTAATTAAGTGAAGAAATTTGAAGAACTCCCGAAATCAAGGCA
 GAGAAATTAAGAGTGAATTTGAATAAGTGAAGTGAAGAAAGTGAAGAAATTTGAAGAAATTTGAAGATGACATCAG
 AAGACATCTATTAGAAATGTACATTTATGATGGGAATGAATGAACATTTATCTAGACTTGCATGTGATCGCCA
 GAATTTCTACAGCATCGTGGAATTAAGAGGCTTGAACCTTTTCTGAAGCGCGGTTTGAATAATATTTA
 GACTTTGACAGCTATAAATATGTTTACACATGAGAAACAGAAATAGACTCATCATGTATTTCTTATTTGCT
 TTTAACAACTTTAAAAAATTAAGAGATTTAGCTCAGAGCCATACAAAATAGAGTGTACATGCTCAATG
 GACCATAGATGCTGTGCCCTCGACGGACTTATAATGTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
 ATCTACATAAATGTCTAAGTTGTAAAGCTCCACTTCCCTTCAAGTTTTCGTCGACCTGAAAGAGGTAACT
 TAGTTTTCGTGCTCACTTGTCTCTCAAAAATGCTATCCCTAACCATATATTATATTCGTTTAAAAACCCCAT
 TAGTGTGGCACAGTAAACACCTGTATGCTGTATTTATGAGGAGATCTCTCATGTTTCTTCTCTCTCA
 AAGTTGAAAAAATGCTTTAAATTTTTCACGCGCGGAAACAGTGCAGCAGTATATGTCGACAGTAAAGTACAC
 AAATTTGAGCACAGTAAGTGCACAAATCTGTAGTTTGTCTGTATCATCCGAGAAACCTGAGGGGAAAAAATTA
 TAGCAATTAATCTGGGATCTGTAGAGTATCCATAAATATGTTATCAAGTATTAGAGTTCTATATTTAAAGATATA
 TGTGTTCAATGATTTTCTGAAATTTGCTTTCTATAGAAATTTCCCACTGATAGTTGATTTTGGAGGCATCTAAT
 TTACATATTTGCTCTTCAAGCTTTGTTTGTACCTGTATCCCTTTATTAATTTGAGTTTCTTCTCATAGTTTGG
 TTTTCTCACTCTCGCAGCTATTTATATTTCAAATAGGAAAAATTACTTTACAGGTTGTTTATCTGTAGCTTAT
 AATGATCATGTAGTTATTCAGTTATCTAGTTTACTGTCTCAGAGGCTGCCCTTTCTGAGTAAATTTGAGCATATA
 ACTGAAGTTATTTTATAAGAAATCAAGTATATAAATCTAGGAAGAGGATCTTCTAGTTTCTGTGTGTTTGA
 CTCGAAAGTACAAAATTTGTCAAGTAACTGTAGTTGTTTGTGTTTAAATTTCAAGTGTACAGAAATGTTAAAAAT
 CCAATCAGTCAAAAGAGGTCAATGAATTAAGAGGCTTGAACCTTTTCAAAAAAAGAAAAA

FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVVLNKDDYIRD LKRIILCF LIVYMAILVGTQDFYSLGLVSKTASSREIRQAFKKLALKL
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLLEDNQGGQYESWNYRYDFGI
YDDDP EII TLERREFDAAVNSGELW FVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKG VNSYPSLFI FRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS
IQTAFAAGIGWLITFC SKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHRRLWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICS NLYVFQP
SLAVFKGQGTKEYEIH HGKKILYDILAFAKESVNSHVTTLG PQNFPPANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVFNQSN IHEYEGHHS
AEQILEFIEDLMNP SVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTDLTPQT FSEKVLQGNHWVIDFYAPWCGPCQNFAP EPELLARMIKGVKAGKVDC
QAYAQT CQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLET LRNQGRNKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAGGACAGAGCAA
GCCATGAACATCATCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGG
GTCGTTGGTGAAGTTTTCATTCTCAGAGGAGAAAACTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTC
CATCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCCTTACCTCATCCC
TATGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACCTTCAGG
GGGAAAACTGGTATCAAACCTCATGTCTCTGCCAGTTTGTGTAATACTGGGTTCCACCA
AAAAATCCAAAGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTG
GATGGAATACTTACCAATAAGAAAAATGATTTTTGTTCCATCGTATATCAATATCTTCTG
ACTACAGAAGTTTCTTCTGAAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCA
TTGAAGCAGTGGTTGGCCACAAAAATCAAATGAAATGAATAAAATAGCTCCAGCCAGAGAT
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTACATTTT
TCAGTCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAA CGAACAGATTA
ATTACCTGTCTTCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGCTGTGTTTTCTT
TCATGCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAAAGTTTTCTTTAAGATAT
TTTATTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGA
AATTTACACAGGGAAGGTTTAAAGCTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAAGATTCAGCATTGAAAGATTCCCTAGCCTCTTCTTTT
TCATTAGCCCAAAACGGTGCAACTCTATTCTGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACAAAAGTGGACCCTCTATATTTCTCCCTTTTATAGTCTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAAGTCTAGCCCCATGA
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAGCTAAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAA
CAATGGACCAAGAGAAGAA

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESIVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTFYFAKRQSI
LVLWDINKRGVEETAABECRKLGVTAHAYVVDCSNREEIYRSLNQVKEVGDTVIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVVFVNTGFTKNPSTRLWPVLETDEVVRSLLID
GILTNNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCACGACAGG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGGCCAGCCCGCCGGGGC
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGTGGGGTGGTGTTCATGATCCT
GCTGATCATCTGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCTTCT
CTAGGCCGACACGGGGCCGCGCTGCCACGCCCAGGGCCGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTGCACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCAGAAAGGAGACGGAGCAGCCGCTGCGCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCAGCGCCGCGCAGCCAGACCAGGGCCGCGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCGCTGCGCATCCGCGCGAGCA
CGTGACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCTGTCGCGACCCC
TTCGTGCGCCTGATCTCCGCCTTCCGAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTGCGCGTGCCCATGCTGCGGCTGTACGCCAACACACAGCCTGCCCGCTCGGCGC
GCGAGGCCTTCCGCGTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGCGAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCCGAAAACCTCCTCC
GAGACTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCTGGAACTGACGCACGCGCACTCC
AGTTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTGTTCACCTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTCAGGTATTTAATACGA

FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGVSFMILLIIVYWDSAGAAHFYLHTSF SRPHTGPPLPTPGPDRDRDELTA
DSDVDEFLDKFLSAGVKQSDLP RKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFTP KERAFFDDIPNSEL SHLIVDDRHGAIYCYVPKVACTNWKRMIVLS
GSLLRGAPYRDPLRIPREHVHNASAHLT FNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELENE EFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLD EDAQLQLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVFLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

FIGURE 195

TCGGGCCAGAATTTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGC GC
GCCTTCGTGAACAGCGGGGCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTTGGCCGCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCACAGAGGCCTGAGGAGACCTCTGCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCCTAGGGCCACAATCCGAGAGGGCATGTGTCGCCAG
CCACTGGGCCCGATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTCTCTGGCCTCCGA
AGCCAACCTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGACAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCCGATATCCCTTCCTGAATTTCTCTCATTT
CTACTTGGGGCCCCCTTCCTAGGACTCTCCACCCCAAACCTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT
AAAAACGATTTGCAGCC

FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFNHSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLLVSETIRRFGRLLDCVNNAGHHPPQRPETSAQGFRLLELNLGTYTLTKL
ALPYLRKSQGNVINISLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVLTGG
AELGYGCKASRSTFPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGACAGCTTGGCGGAATGGACTGGCCTCACAACTG
CTGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA
GAGGAAGGGCAAGGGCGCCTGGGCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTACGGATGA AACCGTATGCCCCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCAGAGAAAGTGTGAGGTCAACTTGACAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCC
GTATCCCCGTGGACCTGCCGAGGCACGGTGCCCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCCGTGTTCAGCCAGGTTCTCTGTGCGCCGCCG
CCTCTGCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGA
CCATCCTCCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA
GCAAG

FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCL
GCVNPFMTQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETI AVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

FIGURE 199

GC GCCGCCAGGCGTAGCGGGGTGGCCCTTGCCTCTCCCGCTTCCTTGAAAAACCCGGCGGG
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG
GCGCCCAACATGCGGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGCGCGCTGGAT
CGCGGCTGTGGCGGCGACGGCAGGCCCCGAGGAGCGCGCTGCCGCGGAGCAGAGCGGGG
TCCAGCCCATGACCGCCTCCAAC TGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
TACGCCCCATGGTGTCCATCTGCCAGCAGACTGATT CAGAATGGGAGGCTTTTGCAAAGAA
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACAGGTTTGATGTG
GCCGCTCTTTGTGACCACCTCTCCAGCATTTTTTCATGCAAAGGATGGGATTATCCGCGGT
TATCGTGGCCAGGAATCTTCAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAATCCCCAGCTTCTTAACGATGCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGACTCTTGGAATT
CCTGCTTGGTGTCTTATGTGTTTTTCGT CATAGCCACTTGGTTTTTTGGCCTTTTTATGGG
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
GAGGAAAGAGATGATTCAAATGAAGAAGAAAAACAAAGACAGCCTTG TAGATGATGAAGAAG
GAAAGAAGATCTTGCGGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCAGC
TGACACAGAGGTGGTGAAGACTCCTTGAGGCAGCGTAAAGTCAGCATGTGCACAGGGGAC
TG TAGATTAAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTGAGCTTCCCTTTGG
CCTGCAGTTTGTACCAATCCTTAATTTTTCTGAAATGAGCAAGCTTCTCTTAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT
GACAAATCAGGATATAGAAAAACAACGTAGTGTGGGATCTGTTTGAGAGACTGGGATGGGAA
CAAGTTCAATTTACTTAGGGGTGAGAGAGTCTCGACAGAGGAGGCCATTCCAGTCCTAATC
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGATCCTTTCTTGTGTAAAGTATTTAT
TTTTGTCAAATTCAGGAAACATCAGGCACCAAGTG CATGAAAAATCTTTACAGCTAGAA
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTATTCTTACCTTTAATTTTTTCCAGCATTTCCACCATGGGCATT CAGGCTCT
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTGTTCATTCTGACCTAAGGGGTTAGATAATCAGTAACCATAAACCCCTGAAGCTGT
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT
TTACAAGACAGATTAAAAAAAATGTTTTGTCCAAATATAGTTGTGTTGATTGTTTTTTT
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCTCTAAGTCTTGCCAGTACAAGGTAGT
CTTGTAAGAAAGTTGAATACTGTTTTGTTTCATCTCAAGGGGTTCCTGGGTCTTGAAC
TACTTTAATAATACTAAAAAACCACTTCTGATTTTTCTTCAAGTGTGCTTTTGGTGAAA
GAATTAATGAATCCAGTACCTGAAAGTGAAAGATTGATTTTTGTTTCCATCTTCTGTAATC
TTCCAAAGAATTATATCTTTGTAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG
GCTAATTTCTTT

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAA VAATAGPEEAALPPEQSRVQPM TASNWTLVMEGEWMLKFYAP
WCPSCQQT DSEWEAF AKNGEILQISVGKVDVIQEPLSGRFFVTTLPAFFHAKDGIFRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVIS ECFYVPLPRHLSE RSEQNRRSEEAHRAEQLQDAEE EK
DDSNEEENKDSLVDDEEEKEDLGDEDAEEEEEEEDNLAAGVDEERSEANDQGPPGEDGV TRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRK SQHADKGL

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAACTCCGGTAAGTACCTAGCCCATGATT
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAGAGCTCC
CAAAATGCTATATCTATTACAGGGGCTCTCAGAAACAATGGAATATCATCTGATTTAGAAAAAT
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACAGGATAGCTGT
TGTTTTAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTGGGTACCATGGGGGTTCTTTCC
AGCCCTTGTCTCTTAATTGGATTATATATGAGAAGAGCTGTTATCTATTAGCATGTCACT
AAATTCCTGGGATGGAAGTAAAGACAATGCTGGCACTGGGCTCTAATCTCTCAAAGATAG
ACAGCTCAAAATGAATTTGGGATTTATAGTAAAAACAAGTGTCTTCCCAACCTGATAATTCATTT
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAACTTATTTTTCAGATCAGAACCCAGCTACCCAAAGAAAAACCATCTCCAAATTTGTG
TATGGATTACAGTGTCACTCATTTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
GAGAAGAAGTTTTCAATGTAAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAAATG
TTAGAGAGCTTTGGCCAACTGTAATCTTAACCAAGAAATGAAGGAGAGGCTGTGATTTCT
GTATTTGTGCGACCTACAGGTAGGCTAGTATTATTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAAGCTTGAGTTTTATTTTTTATTTATTTATTTTTTGGATAGGGTCT
CACTTTGTTACCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGTATCTCTCGC
CTCAGCCCCCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTG
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCTCGGGGTTAAG
TGATCTGCCCCCTTGGCCTCCCAAAGTGTGGGATTACAGATGTGAGCCACCACACCTGGC
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTTACCTTGGGTAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGACCGT
GTGTTGCCACGATTTGACCCTCAACTCTAGCAGTATATCAGTTATGAACGAGGGTGAAT
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAATCTTCACCACAGTCAGAGCAATTTT
ATTATTTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACCTCTTA
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAAATCTTT
TTTTTTTTTTTTTTTTTTTTTGAGACAGAGTTTCGCTCTTGTGTCACAGGCTGGAGTGCAACGG
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTTCTCTGCCCTCAGCCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCCACACCCCGGCTAATTTTGTATTTTTTTAGT
AGAGACAGGTTTTCTCCATGTGCGTCAAGGTAGTCCGAACTCCTGACCTCAAGTGATCTGC
CTGCCTCGGCCTCCCAAGTGTGGGATTACAGGCGTGAGGCCACTGCACCCAGCCTAGAATCT
TGATAATATGTAATTTGAGGAAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA
AAAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
ACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT
ACCAATTTTTTTCAGTAATTAACGTAAAAATGGTATTTATGGAATGAACATATATTTCTCATG
TGCTGATTTGTCTTATTTTTTTCATACTTTCCCACTGGTGCTATTTTTATTTCCAAATGGATA
TTTCTGTTATTACTAGGAGGCATTACAGTCTCTAATGTTGATTAAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATTAATGCAGTTTTAAATGGATGATTTTATGTTTATGTGGATTTCAT
TTCATAAAAAAAACCTCTTATCAAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDEGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSPPCPNWIIEKSCYLFMSLSNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSNVCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

[illegible]

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MT PQSLLQTTFLFLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFFLLSDKASSLLCFQH
QEE SLAQGPPLLATSVTSWWSPQNI SLPSAASF TFSFHSPPHTAAHNASVDMCELKRD LQLL
SQFLKHPQKASRRPSAAPASQQLQSLESKLT SVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKANLTEPVVLT FQHQLQPKNVTLCQVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVL MVSSVEVD AVHKHYLSLSYVGCVV SALACLVTIAAYLCSRVP LPC
RRKPRDYTIKVHMNLLLAVFLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE
GYNLYRLVVEVF GTYVPGYLLKLSAMGWGFPI FLVTLVALVDV DNYGPI ILAVHRTPEGVIY
PSMCWIRDSLVS YITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVLTLLGLSLVLG
LPWALIFFSFASGTFQLVVL YLFSIITSFQGF LIFIWYSMRLQARGGPSPLKSNDS SARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGAGA
GGAAANCNTCGGGACTACACCNCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTCCTGTTCAACATGG

FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCCAGGTCCAGGTTTTCGCTTTGA
TCCTTTTCAAACCTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTGGATGGGATTTATGTGGAACTACCCCT
AGGATTTCTGTGCGACGACGAGGCTCGGCGCTTCCACCCCACTGGCAGCTTCCCTGGCGGTGGTGAAGAGAC
TCCGGAGTCCGTGCTTCCAAAGTGCCTCCGCGGTGAGTGAAGCTCTCACCCCACTCAGCCAAATAGAGCCTCTTCGGGG
TTCTCTCTGTGAGCTTGCCTTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACTTGATAGTAAATCC
AGTTTTCCAGCAACAGGAACAGAAGCGAGTACAAGATCCCTCAGCATGAGAGAAATTATTACTGTGTCTACTAATG
GAGTATTTACAGCCCAAGGTTTCTCTCATCTTATCCAAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
AGGAAATGTGTGATACAACCTTACGTTTGTATGAAGATTTGGGCTTGAAGACCCAGAAGTGCATATGCAAGT
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAATATATTAGGCGCTGGTGTGGTCTTGGTACTGTACCCAG
GAAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTCTGTGAACCAAGGT
TCTGCATCCACTACAACATTGTCTATGCCAACATTCACAGAAGCTGTGAGTCTTCAAGTGCTACCCCTTCAGCTT
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGAGCTTATTTCGATATCTTGAACCAAG
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTCTTGGCAAGGCTTTTGTTTTTGGAA
GAAAAATCCAGATGGTGGATCTGAACCTTCTAACAGAGGAGGTAAAGATTACAGCTGCACCTCGTAACTTCT
CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTG
GTGGGAACCTGTGCTGTTGTCTCCAAATTTGCAATGAATGTCAATGTGTGCCAAGCAAAGTTACTAAAAAATACC
ACGAGGTCTCTCAGTTGAGACCAAAGACCGGTGTGAGGGGATGCACAAATCACTCACCAGCTGGCCCTGGAGC
ACCATGAGGAGTGTGACTGTGTGTGACAGGGGAGCACAGGAGGATAGCCGCATCACCACAGCAGCTCTTGGCCA
GAGCTGTGCACTGAGTGGCTGATTCTATTAGAGAACGATGCGTTATCTCCATCTTAACTCAGTTGTTTGTCT
TCAAGGACCTTTTATCTTCAGGATTACAGTGCAATTCGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA
ACAGCTCTTTTGTAGAGGAGGCTTAAAGCAGGAGAGAAAGGCTCTCAATCGTGGAAAGAAAAATTAATGTGTAT
TAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTCAGTGGGTTCTGTATTTTCAAGTTCTTTT
GATACGGCTTAGGATGATGTGAGTACAGGAAAAAAGCTGTGCAAGTGAGCACCTGATCCGTTGCCTTGCTTAAC
TCTAAAGCTCATGTCTCCGGGCTTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTGTCTCATATTCACAT
ATGTAAACAGAACATTCTATGTACTACAACTCGGTTTTTAAAGGAACTATGTTGTGTATGAATTAACCTTGT
GTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAGTTTCTGCCATTAGAAGAGAGAACTACA
TTCATGGTTTGAAGAGATAAACCCTGAAAAGAGAGTGGCCCTATCTTCACTTTATCGATAAGTCAGTTTATTTG
TTTCAITGTGACATTTTATATCTCCTTTTGACATTATACTGTGGCCTTTTCAATCTTGTAAATATATCT
ATTTTAAACAAAGGTATTTAATATCTTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAATTTTCT
AAACACAATGTTATAGCCAGAGGAACAAAGATGATATAAAATTTGTTGCTTGACAAAAATACATGATTTTCA
TTCTCGTATGGTGCTAGAGTAGATTAATCTGCATTTTAAAAAAGTGAATTGAATAGAATTTGAAGTTGCAAA
GACTTTTTGAAAAATTAATAATATCATATCTTCAATTCCTGTTATTGGAGATGAAATTAAGCAACTTATGA
AAGTAGACATTCAGATCAGCCCATCTAACCTATTCTTTTTTGGGGAATCTGAGCCTAGCTCAGAAAAACAT
AAAGCACCTTTGAAAAGAGCTTGGCAGCTTCTGATAAAGCTGCTGTGCTGTGCATGAGAAACACATCTTTA
TTGTGATGTTGGTTTTTATTATTTTAAACTCTGTTCCATACCTGTGTATAAATACATGATATTTTATGTACA
GAAGTATGCTCTTAACCACTGCTATTTGTACTCTGGCAATTTAAAGAAAAATCAGTAAAAATTTTGTCTGT
AAAAATGCTTAATATNGTGCTAGGTTATGTGGTGACTTTTGAATCAAAAATGTATTGAATCATCAAATAAAG
ATGTGGCTATTTTGGGAGAAAAATTAATAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTATCGCGCC

FIGURE 207

MSLFGLLLTSALAGRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRKSRVVDLNLLEEVRLY
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNEQCQVPSKVTKKYHEVLQ
LRPKTGVVRGLHKSLTDVALEHHEECDVCVRGSTGG

Signal sequence:

amino acids 1-14

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACGAGACCTCTACATTCATTGGAAGA
 AGACTAAAAATGSGTGTTCCTAATGTGGACACTGAAGAGACAATTCCTATCCTTTTAAACATAATCCTAATTTCC
 AAACCTCTTGGGGCTAGATGGTTCTCTAAAACCTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG
 ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATCCCAAGAACCCAGAACCTCACCTCTC
 ACCATTAACCATATCCAGACATCTCCCGAGCGTCTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCAGA
 TGCAACTGTGTACCTTATCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAACCCAGAAAGC
 TTTAGTGGACTCACTTATTTAAAAATCCCTTTACTGGATGGAAACAGCTACTAGAGATACCCGAGGGCCTCCCG
 CCTAGCTTTACAGCTTCTCAGCCTTGAGGCCAACAACTCTTTCCATCAGAAAAAGAGATCTAACAGAACTGGCC
 AATCAAGAAATCTCTACTCTGGGGCCAAACCTGTATTATCGAAATCCTTGTATTGTTTCAATTAATAGAGAAA
 GATGCTCTCTAAACCTTGACAAAGTAAAAAGTGCTCTCCCTGAAAGATAACAATGTCAAGCCGCTCCCTACTGTGT
 TTGCCATCTACTTTAACAGAACTATATCTCTCAACAACATGATTGCAAAAAATCCAAAGAGATGATTTTAAATAAC
 CTCAACCAATTACAAATCTTTGACCTAAGTGGAATTCGCCCTCGTGTGTTAATGCCCCATTTCTTGTGCGCG
 TGTAAAAATAATCTCCCTACAGATCCCTGTAAATGCTTTTGTGCGCTGACAGAAATTAAGGTTTAACTGCTA
 CACAGTAACCTCTCTCAGCATGTGCCCCCAAGATGGTTTAAGAACATCAACAACTCCAGGAATCGGATCTGTCC
 CAAAACCTCTTGGCCAAAAGAAATGGGGATGTCTAAATTTCTGCAATTTCTCCCCAGCCTCATCAATTTGGATCTG
 TCTTTCAATTTGAACCTCAGGTCTATCGTGCACTATGAATCTATCAACAGCATTTTCTTCACTGAAAAGCCTG
 AAAATTTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAGCTTTAAACCTCTGCCATTACATAATCTTCAA
 AATCTTGAAGTCTTTGATCTTTGGCACTAACTTTATAAAAAATGTCAACCTCAGCATGTTTAAACAAATTTAAAGA
 CTGAAAGTCAATAGATCTTTTCACTGAATAAATATCAACCTCAGGAGATTCAGTGAAGTTGGCTTCTGCTCAAT
 GCCAGAACCTTCTGTAGAAAAGTTATGAACCCAGGTCCTGGAAACAAATTAATTTTCAATATGATAGATATGCA
 AGGAGTTGAGATTCAAAACCAAGAGGCTCTTTTCTGATGTCTGTTAAGTAAAGCTGCTCAAGTATGGGCGAGCC
 TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCCCTGATTTTTCAGCATCTTTCTTCTCACTGAAAAGCCTG
 AATCTGTGAGGAAATCTCATTAGCCAAACCTCTTAATGGCAGTGAATTCACACCTTTAGCAGAGCTGAGATATTTG
 GACTTCTCCAAACACCGCTGTGATTTTACTCCATTCACAGCATTTGAAGAGCTTCAACAACTGGAAGTTCTGGAT
 ATAAGCAGTAAATGACCATTTATTTTCAATCAGAAGGAATTAATCATATGCTAACTTTACCAAGAACCTTAAGGTT
 CTAAGAAACCTGATGATGATGAACGACAAATGACATCTCTCTCCACAGCAGGACCATGAGAGATTTCCAACTGTCTC
 ACTCTGGAATTCAGAGGAATCACTTTAGATGTTTATGTGAGAGAAGGTGATAACAGATATCTACAATTTATCAAG
 AATCTCTTAAATTTAGAGAAATAGACATCTCTAAAAATTCCTAAGTTTCTTGCCTCTGGCTTTTGTATGCT
 ATGCTCCAAATCTAAGAAATCTCTCTTGGCCAAAATGGGCTCAATCTTTCACTTGGAGAAATCCAGTGT
 CTAAAGAACTGGAACTTTGGACCTCAGCCACAACCACTGACCACTGTCCCTGAGAGATTTCCAACTGTCTC
 AGAAGCCTCAAGAACTGATCTTTAAGAAATAATCAAACTCAGAGTCTGACGAAGTATTTTCTCAAGATGCTCTC
 CAGTTGCGATATCTGGATCTCAGCTCAAAATAAATCCAGATGATCAAAAGACACAGCTTCCCAAGAAATGCTCTC
 AACAACTGGAAGATGTGCTTTTGCATCAATAATCGGTCTTGTGCACTGTGATCTGTGTGTTTGTCTGTGTG
 GTTAACCACTACGAGGTGACTATTCCTTACTTGGCCACAGATGTGATCTGTGTTGGGCCAGGACACAAAGGC
 CAAAGTGTGATCTCTCCTGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATCTGTCTCTCACTTTCCATA
 TTTCTGTATCTCTTTCTCATGGATGATGACAGCAAGTCACTCTATTTCTGGGATGTGGGTATATTTACAT
 TTTCTGTAGGCCAAGATAAAAGGGTATCAGCGTCTAATATCACAGACTGTGTGCTATGATGCTTTTATGTGTAT
 GACATCTAAGGACCCAGCTGTGACCCGAGTGGGTTTGGCTGAGCTGTGTGGCCAACTGGAAGACCCAGAGAGAAA
 CATTTTAAATTTAGACAGTGTTTTGTGATGACAGCAAGTATGCAAGACTGAAAATTTTAAAGATGACATTTTAC
 TTGTCCATCAAGAGCTCTGGATCGAGATGAAAAGTTGATGTGATTTATCTGTATTTCTTGAAGGCCCTTTCAAGAG
 TCCAGATTTCTCTCAGCTCCGAAAAGGCTCTGTGGGAGTCTGTGCTTGTGATGGCCAAACCAACCCGAGCTCAC
 CCATCTCTGCACTGTCTAAGAACGCCCTGGCCACAGACATCATGTGGCTATAGTCAGGTGTTCAAGGAA
 ACGGCTTACGCCCTCTTGTGAAAACACAACCTGCTAGTTTACCAAGGAGAGGCTGGC

FIGURE 209

MVFPMTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG
IPTNTNTNLTLTINHIPDISPASFHRLDHLVEIDFRNCNCPPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEIILYLGNQCYR
NPCYVSYSIEKDAFLNLTCLKVLSLKDNNTAVPTVLPSTLTLYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLSKSL
KILIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ
TLDLSKNSIFFVKSSDFQHLSPFKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKMMNDNDISSSTSRTMES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL
AKNGLKFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSKLNILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHNRFLCTCDAVWFVWVNVNHTVETIP
YLATDVTCVGPAGAHKQGSVISLDLYTCELDLTNLILFSLSSISVSFLFMMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLCL
RDWLPQGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHYPFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

FIGURE 210

GGGTACCATTCTGCGTGTGCTCAAGTTACGGAATGAAAAATTAGAACACAGAAAAATGGAAAAATGTTCTCTTC
AGTCGTCGAATGCTGACCTGATTTTCTCGCTAATATCTGGTTCCGTGTGAGTTATGCGCGGAAGAAAAATTTTCTTA
GAAGCTATCCCTTGTGATGAGAAAAAGCAAAATGACCTAGCTATTGCGAGAGTGCAGCAATCGTCGACATCGGAAG
TTCCCCCAACCGTGGGCAAAATATGTGACAGAACTAGAACCTGCTGATAATTTTCATCACACATCAACGAATGAAT
CATTTCAAGGGCTGCAAAATCTCACTAAAAATAATCTTAACCAACCAACCCCAATGTACAGCACAGACGGAATTC
CCGGTATACATCAATAGGCTTGTATATACAGACGGGGCATTCCTCAACCTTAAAAAATCACTAAGGGAGTTACTGCT
TTGAGACAGCAACAGTTACCCCAAAATCCCTCTGGTTTGGCAGAGTCTTTGACAGAACTTAGTCTAATTTCAAAACA
ATATATAACAACATAACTAAGAGGGCATTTCAAGACTTATAAATCTGAAAAATCTCTATTTTGGCTGGAACTGCT
ATTTTAAACAAAGTTTGGCAGAAAACTAAACATAGAAGATGGAGTATTTGAAACCGCTGACAAATTTGGAGTTGCTAT
CACTATCTTTCAATTCTCTTTCAACAGCTGCCACCCAACTGCCAAGCTCCCTACGCAAACTTTTCTGAGCAACA
CCGAGATCAAAATACATTAGTGAAGAAGATTTCAAGGGATGTATAAATTTAAACATTACTAGATTAAAGCGGGAAC
GTCCGAGGTGCTTCAATGCCCATTTCCATGCGTGCCCTGTGATGGTGGTGCTTCAATTAATATAGATCGTTTGT
CTTTTCAAACTTGACCCAACTTCGATACCTAAACCTCTCTAGCACITCCCTCAGGAAGATTAATGCTGCTCGT
TTAAAAATATGCCCTCATCTGAAGGTCTGGATCTTGAATTCAACTATTAGTGGGAGAAATAGTCTCTGGGGCAT
TTTTAACGATGCTGCCCGGCTTAGAAATACTTGACTTGTCTTTAACTATATAAGGGGAGTTATCCACAGCATA
TTAATATTTCCAGAAACTCTCTAAACTTTTGTCTCTACGGGCATTCGATTTAAGAGGTTATGTGTCCAGGAAC
TCAGAGAAGATGATTTCCAGCCCTGATGAGCTTCCAAACTATCGACTATCACTTTGGGTATTAATTTTATTA
AGCAAAATCGATTTCAAACTTTTCAAAATTTCTCCAATCTGGAATTAATTTACTTTGTCAAGAAAACAGAAATACAC
CGTTGGTAAAAGATACCCGGCAGAGTTATGCAAAATAGTTCTCTTTTCAACGTCATATCCGGAACAGAGCTCAA
CAGATTTTGAAGTTTGACCCCAATTCGAACTTTTATCATTTTACCCGCTCTTTAATAAAGCCAACTTGAAGTGTCT
ATGGCAAGGCTTAGATTAAAGCTCAACAGTATTTTCTTCAATTGGGCCAAACCAATTTGAAAACTTCTCTGACA
TGTCCCTGTTTAATCTGTGTCGAAATAGCAATGCTCAAGTGTAAAGTGAACATGAATTTTCCAGCACTTCCCTATG
TCAAAATTTTGGATTTGACAAACAAATAGACTAGACTTTGATAAAGCTAGTGTCTTACTGAATTTGTCGACTTGG
AAGTCTAGATCTCAGCTACAATACACATATTTAGAATAGCAGGGCAACAACATCATAGAATTTATCAAAA
ATTTCAAAATCTAAAGTTTTTAACTTGAGCCAAACAACTATTTATCTTTAACAAGATAAGTATAAATCTGAAA
GCAAGTCCGCTGATAGATTGTTTTCAGTGGCAATCGCTTGACATTTTGTGAATGATGATGACACAGAGTATA
TCTCCATTTTCAAAGTCTCAAGAACTGACACAGTCTGGATTTTATCCCTTAAATAGGCTGAAGCACTCCCAATG
AAGCATTTCCCTAATTTGCCACGAGTCTCACTGAATACATATAAATGATAATATGTTAAAGCTTTTAACTGGA
CATTAATCCACAGCTTTCCTCGCTCGAGTTGCTTGACTTACGTGGAACCAACTATCTTTTTAACTGATAGCC
TATCTGACTTATCATCTTCTCGTCCGACACTGCTGCTGACTATACAGGATTTCCCACTACCTCTGGCTTTC
TTTCTGAAGTCAAGTCTCGAAGCACTCGATTTAAGTTTCCAATCTGCTAAAACCAATCAACAAATTCGCACTTG
AAACTAAGACCAACCAAAATATCTATGTTGGAATACACGGAACCCCTTGAATGCACTGTGACATTTGAG
ATTTCCGAAGATGGAATGATGAACATCTGGAATGTCAAAATTCAGACATGATAGATGTCAATTTGCGCAGTCTG
GGATCTAAAGCAGGAAGATATTGTGAGTCTGGAGCTAACAACTTGTGTTTCCAGATGTCTGAGTGATATATT
TTTTCTTCAAGTCTTTATACCAACATGGTTATGTTGGCTGCCCTGGCTCACCTTTGTTTACGTGGATGTTT
GGTTTATATAATATGTGTTTGAAGTAAAGGCTACAGGTCCTTTCCACATCCCAAACTTTCTATGATG
CTTACATTTCTATGACACCAAGATGCTCTGTGTTACTGACTGGGTGATAAATGAGCTGCGATCAACCTTGAAG
AGAGCCGAGACAAAACTGCTTCTTGTCTAGAGGAGAGGGATTTGGGACCCGGGATTTGGCCATCATCGACAAAC
TCATCGAGACATCAACCAAGCAAGAAAAACAGTATTTGTTTAAACCAAAATATGCAAAAAGCTGGAACCTTTA
AAACAGCTTTTACTTGGCTTTGACAGAGCTAAATGGAATGAGAACATGGATGTGATATATTTATCTGCTGGAGC
CAGTGTATACAGCATCTCAGTATTTGAGGCTACGGCAGCGGATCTGAAGAGCTCCATCTCCAGTGGCTGACA
ACCCGAAGGCGAGAGGCTGTTTGTGGCAACTCTGAGAAATGTGGTCTTGATCGAAATGATTCCAGGTATAACA
ATATGTTATGCGATTTCCATTGAAGCAATACTAACTGACGTTAAGTCATGATTTGCGCCATTAATGAAGTGCACAA
GAATGACATTTCTGATTAGTTATCTATGCTATGTATGTAACAAATATCCCAAACTTAGTGGTTTAAACCAACA
TTTGTCTGGCCCAAGTTTGTGAGGCTCAGGAGTCACGGCCAGCATAACTGGGTCTCTGCTCAGGCTGTCTCAG
AGGCTGCAATGTAGGTGTTTCAACAGAGACATAGGCACTCACTGGGCTCACACTCATGTGGTGTGTTTCTTGAATCA
ATTCTCTCTGGGCTATGCTGCAAGGCTATACATCATGTAAGCCATGCGAGCTCTCCAGGAGTGCAGTTGCTTC
ATCAGAGTAGCAAAAAGAGAGGTTGTAGCAAGATGAAGTCAAACTTTTGTAACTGAATCAAAAAGATGAT
ATCTCATCACTTTGGCCATTTCTATTTGTGAAGTAAACCAAGTCCCACAGTCCATGCGGAGTGCACACC
TCAGTCTCAGGAAAAACAGCTGAGGACCAAGATGGTGAAGCTCTGATGCTTCAAGTTGTCATCAACTTTTTCCT
TGACTGCTGTCTGGGATGGCTGATCTCTGATGATAGATTGGAATATCAGGAGGAGGATCACTGTGGGAC
ATCTTAGCAGTGTGACCTAACACATCTTTTCAATCATTAAGAACTTTTGGCACTGTGACTATGGTCTCTAATA
TTAAGCTGTGTTTATATTTTATCATATATCTATGATGCTATGTTATATTTATGCTGTGGTGTGGTGTGTTTAT
TTACAGTTGCTTTTACAAATATTTGCTGTAACTTTGACTTCAAGGTTTGAAGTGCATTTAAGAACATGAGATG
ATAGCTTTTAAAGCATCTTTTACTCTTACCATTTTAAAGTATGTCAGCTAAATTCAGAACTTTGGTCTATA
TTGTAAATTGCCATTGCTGTAATCTTAAATGAATGAATAAAATGTTTCAATTTTCAAAAAA

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSPCDEKKQNDSVIAECSNRRLQEVPTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLHNPNVQHONGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTELSQLNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL
TLLDLSGNCPRCFNAPFPVPCDGGASINIDRFQNLTLQRLYNLSSTSLRKINAAWFKNM
PHLKVLDFEYNLVGEIVSGAFLTMLERLEILDLSFNKSYQPHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFNLEIIYLSENRISPLV
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACNLNSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDEV
LDLSYNHYFRIAGVTHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWNDDDNRYISIFKGLKNLTRLDLSLNLKHIPNEAFLNLPASLTELHINDNMLKPFNWT
LLQQFPRLELDLDRGNKLLFLTDSLSDFTSSLRTLLLSHNRI SHLPSGFLSEVSSLKHLDSL
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFFFITTMVMLAALAHHLFYWDVWFYINVLAKVK
GYRSLSTSQTIFYDAYISYDTKASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIIID
NMQSINQSKKTVPVLTKKYAKSWNFKTA FYLALQRLMDENMDVIIIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGFLWQTLRNVLVTENDSRYNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTC CCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGTGC AAGGGAGGCTCCTGTGGA
CAGGTCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGC
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCAACCCGGAGGA
GCAGTCTCTGCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCTGAGGGCACAGGCCATGAGGGGCTCTCAGGAGTGTCTGTGATGTGGCTT
CTGGTGTGTGGCAGTGGGCGGCACAGAGCAGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCAGGGGACCTGTCTCCGAGTCGTTCTGTGAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGCCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCTGCCAGGCCTCGCTACGCGTGTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCGAGCGCCATGCGGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCAGTCA
GATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAA
GAAGTGACAGAGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC
CCCACTGCACAGCCTGGCCTCGCAGGCCTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGCACTCCTTCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTCTCTTCTGTG
GAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGACCTGCCAGCGCCCCAGGGTG
GACTGAGCCCCTCACGCGCCCTGCAGCCCCATGCCCTGCCCAACATGTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTCTTCTCTCTCCCC
TTCTCGGGAGGCTCCCCAGACCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCTGGCTACCCCAACGGCATCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCTGTCTGGAGCTGGGACCCATGGCACAGGCCAGGCAGCCGGAG
GCTGGGTGGGGCTCAGTGGGGGCTGTGCTGACCCCCAGCACAATAAAATGAAACGTGA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLITCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

FIGURE 214

GCCAGGCAGGTGGGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCGTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCACGGGGGCCCGGGAGGGGAACGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTC
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCTAGGGTGTGTGCTGTCCGGGCTACGGGGACCTGTCTCCGAGTCGTTCCG
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGAGCCCTGGGCTGGCCCTGCAGGCCTCGCTA
CGCGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCTGTGGAGCAGCAATAT
GCCAGCCGCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGTGCCGTGCCCTGCA
GGATGGCGGGGTGACACTTGCAGTCAGATGTGGATGAATGCAGTGTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACCTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACCTCTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCTTCTTGAGGAGCAGCTGGGTCTGCTCCTGCAAGAAAGA
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCTCACGCCCTGCAGCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCTCTCTTCTCTCTCCCTTCTCGGGAGGCTCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTGTGAATCCACCCTGGCTACCCCCACCTGGCTACCCCAACGGCA
TCCCAGGGCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGCTGCTGCTGAC
CCCCAGCACAAATAAAATGAAACGTG

FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQSDVDECSARRGGCPQRCINTAGSYWCQWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCTCAGGAGGTGCTCCAGGCGGCCAGTGGGCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGCTCCAGCAGCAT
CAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCAATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGC
AGTGGGCGGCACAGAGCACGCGCTACCGGCCCGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCTCACCACCTGCGAC
GGGCACCGGGCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
GCTGGCCCTGTCAGGCCTCGCTACGCGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGCTGTGTGGAGCAGCAATATGCCAGCCGCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGTGCGCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGTAGGAGGGGCGGCTGTCCCAGCGTGTGCTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGG
CCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGACCCCGGCAGCCTCCTGGTGCCTCC
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTCTCTTCTGGAGGAGCAGCT
GGGGTCTGTCTCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCATGCCCTGCCCAACATGCTGGGGTCCAGAAGCCACCTCG
GGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTCTTCTCCTCCCTTCTCCTCGGGAG
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGGTACC
CCCACCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCCAGCTGAGGGAAGGTAC
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGAGGCTGGGTGGGG
CCTCAGTGGGGCTGCTGCCTGACCCCCAGCACAAATAAAATGAAACGTG

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCFQRCVNTAGSYWCQCWEGHSLSDGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

[illegible]

GGTTGGCCACAGCTGGTTTGGGCCCCGACCACTGGGGCCCTTGTGACGAGGAGGACAGCCCTCCGGGCCGGGGGAG
GACAGAGTGCCTGCCACCTTCCGCTGACGAGTGAATTCCTGGGACAGTCCGTTTACCGCTCTGCGGACCGCGCCGC
AGTTGGGTTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGGTCTTCCCGCTCGGGCCGGTTATTCGGAGAG
AGATTGTTCTCCAGGCTCAGCAATTGGACCTTTGATGATTTGACCCAGCGCCAGGAATAGCAGGCAACCTCGAT
TCAAAGTGGGCTCAGCTCTGTTTCTCTCTCGTGAATCGCAAAACCACTTTGGAGCAGGAATTCCAACTA
GTGCTGTGATGGTGTGGTGAAGAAAGGTGACAGGAATGGGAGAACTCCGAGGACGGAACCACTTTTGCTGT
ATGGCCGGCTCATAGTAGCCCGGAGGAGGCAATTTTCACTGACCTTTTCTCATCTGGGGACATGTGACAT
TCTTTCTGCCTTTGATGGCCGCTACCTGGCTCTTCAGCTGCTCTCTCGCATCCCTGATTTTGTGTCGATGCTCT
TCTCTTTCTCATGGTCTACATCTTTTGAGGACAGCTTCAGTGAACGTGAGTGATCTCTCGGCGCTACCAAGTG
AAGCAGCTTTTACAGAAATGGGATAGGAAGTACCAATGGTGGTGGCTGGCCAGGGCCAGGACGACCTCCGCTGTA
TCAAGAAATTCAGGATAAACACCAAGATTGTGAATCGAAATCTGTACACATCGAAGATTTCCGCGCTCCCC
GGGCTCCCAATCGAGCATCTGTGACAACTGTGGAGCGCTCTGCACATCATCTGCCCTGGGTGGGGAATTTGT
TGTGAAGAAAGGAAATACCGCTACTTCTACCTCTTCACTCTCTCTCTCTCTCTCTCAACATCTATGTTCTGCGCT
TCAACATCGTCTATGTGGGCTCAAACTTTGAAGAAATGGCTCTTGAGGACATGAAGAAAGAACTCTTGGAACT
TCTAGAAGTCTCATTTGCTTCTTTACACTTGTGCTGGCTGGTGGAGTACTGGAATTAATACTTCTCTCGTG
CTCTCAACCGACAGCAACATGAGAGCAATGAAGGATCTGACGACAGGGAAGATCGCTGTCGACGAATCTGACAGCC
ATGGCAATTTGAAGAACTGCTGTGAAGTCTGTGTGGCCCTTGGCCCCAGGTGTGCGATCAGGAGGTA
TTTGGCACTGGAGGAAGTGGAACTGCACTCCCAATGACTCAAGAGACATGACAGCTTCTGCCACAGCC
TAGCCCTTCCGACAACTGAACTCAAATGAGATCGGAGGACAGCAGCATCTCCGCAAGATGATCACTCCAG
AGCCCCAGACCTTCCAGCGAGGCGCTGAAGCTGAGAAGTAGCCCTATCTATGGAAGAGACTTTGCTTGT
TAATTAGGCTATGAGAGATTTCAAGTGGAGAGTTAAACCTGAGACAGAGAGCAATGAAGCTGTGCCCTTTTAAGT
GTCTTTTCTTGGTCTTTAGTACCCCAAGTGCACATGCAATTTCTTGCTCGAAGCTTTTAAATTTCTGAACT
CAGGCGACGACGAAGATGTGATCATCTGTAACTCTGTAATCGAAAGAAATGGGTCTCTGGGCCCTGGCATGCT
TCCATGGCTCAGCAGCAGGCTCCGCTCGACCCCTCTCTCCCTCAGATCCGACCTCTGCTCTGGGGTCACT
TGCTCTCATTTCTGGGGCTAAAAGTTTGTGAGATGTGCTCAAAATCTCCCAAGCTCTGTCAGCTCTGTGATTCAGA
GGCAGTACAGAGACCTCTGGCCAGGGGACTCTAACTGGGTTCTGGGGTCTTCAGCACTGAAGAGAGGAGAG
TGGGTCAGAGAATTTCTCTGGCCACCAAGTGCACGACTGCCACAATCTTTAGGAATGGGACGATGACT
TCACTTTGTGTGTTANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTTGTTTCTTGGACTCTGCTCCATTAGGAG
CAGGAATGGCAGTATAAAAAGTCTGCACTTTGGTCAATTTCTTCTCAGAGGAGCCCGAGTGTCTCACTTAAGAC
ACTATCCCTCAGACTCCCTGTGTGGAGGCTCGACAGGCGCTGATGACCAAAATGGGAAACCAAGGACAGAG
GCTCTCTCTCTCTCTCTCCCGGATGTACCTTCAAAAAGAAAAAATGCTAACAGGTTTCTTCATTAAAGCT
CGGCTGAGTGGAGGAAAGCCGACATCTGCTCGCTCTCGGGTAATCTACCTTAAGGCTCTCGGCCACTCTGTGCT
ATGGTAACCACTCTGGGGGCTTCTCCAGCAGCCGCTCTCTCAGCACTCTACACCGGACAGTACCAAGGACATTC
CACCTCGGGGTTGGCTGTGGCCGCCGCTCAGCTCTGCTCAGGACTGTCTATTTCAGGGAAGGAAGATTTATGT
ATTATATGTGCTCTATTCTCTAGAGCACTGTGTTTCTCTCTTCTAGCAGAGGCTCTCTGCTGATGACTTATG
CGGGTGGGGGAGTGAACCGGAATTTTCACTATTTTGAAGGCGATTAACTGCTCTAATGCA

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFC CDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGN CVGKRNYRYFYL
FILSLSLTLTIYVFAFNIVYVALKSLKIGFLET LKETPGTVLEVLCFFTLWSVVGLTGFHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEA AEAK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

FIGURE 220

AAAACCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCCTTCT
CCCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGAATTGTGTTGGAAAGAGGAATA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

FIGURE 221

GTGTGTCTCTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAGAAAAAGAAAGA
AAAAAATCATGAAAAACCATCCAGCCAAAAATGCACAATTCATCTCTTGGGCAATCTTCAC
GGGGTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCGTGGTACGGAGAGTAAAGGTACCCGTGAACATATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGAAAAACAGACCTTTCTCTCAAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGAACTACACTTGGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCAGGTGAGCAACGGCAGTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCAACACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAGAGTTTTAAAAAGAAATTGAA
AATTGCTTGCAGATATTTAGGTACAATGGAGTTTCTTTTCCCAACCGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGTGCATCGTGCAACCTCTTTGGTGCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTGTGAAACGTGAAATAAAAGAGCAAAA
AAAAA

FIGURE 222

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTI LYAGNDKWCLDPRV VLLSNTQTQYSIEIQNV D VYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYEC SASNDVAAPV VRRVKVTVNYPPYISEAKGTGVPVGQKGTLCCEASAV
PSAEFQWYKDDKRLIEGKKGV KVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGH TNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKF

Signal peptide:

amino acids 1-28

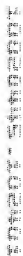


FIGURE 223

GAAAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAATGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

FIGURE 224

ATGGCTGGTGACGGCGGGGCGGGCAGGGGACCGGGGCGCGGCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACCCGCTGGCGCGACTCCACATGAACGCTCGCGCTCGAGGAGCTGGGAGCTGGGAGCAACGTTGGGATTCCAG
AAGGGGACAGACAGCTGTAGGCTCACGACAGCTGGAGCTGGTCTTAGCAGGTGCCCTCTCTACTGCTGGCT
GCACGTCTCTGGGCTGCTTTGGGCCCTAGGGGTCAGTACCAAGAGACCCATCCACAGCACCTGCCCTTACA
GAGGCTGCATTGAGTGGCTGGAAAAATCTGAGTCCCTGGACCGAGGCTGAGCCCTGTGAGGACTTTTAC
CAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
CTCTGGGACCAAAACAGGCCATCTAGAAGCACCTGCTTGAACACCACTTCAACTCCAGCACTGAAGCTGAG
CAGAAGACACAGCGCTTCACTTATCTTGCCACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA
GACCTCATTTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACAGGACCACTTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCCATTTTCAACCGTCTACATCAGTCCGCACTTAAGAGTTTCAACAGC
AATGTATTCAGGTGGACAGCTCTGGCTCTTTCTGCCCTCTCGGATTACTACTTAACAGAACTGCAATGAG
AAAGTGCTCACTGCCCTATCTGGATTACATGGAGGAACCTGGGATGCTGCTGGGTGGGCGGCCCACTCCACGAGG
GAGCAGATGCAGCAGTGTCTGGATTGAGAGATACAGCTGGCCAACTACAGATGCCCGAGGACGAGCGCGGAC
GAGGAGAAAGATCTACCAAGATGAGCATTTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAAGTT
CTGTCTTCTTGCTGTCAACATTGGAGTTGAGTGATCTGAGCGCTTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTCAAGCTCATCAACCGCAGGAACCAAGCATCTGAACAAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACCTCAAGCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCTCTATGGCACTAAGAAG
TCCTGTGTGCCAGGTGGCAGACTGCATCTCAAACAGGATGACGCCCTTGGCTTTGGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTGAACCGCAAAAGCAAAATTTGAGAGGGGATGATCAGCGAAATCCGAGCCGCACTTGA
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGACGGCAGCCAGGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTCCAGACTTTATCTCTGGAGCCCAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTTCCAAACATGTTGAATTTGTACAACCTTCTCTGCCAAGGTTATGGCTGACCACTCCGCAAG
CCTCCAGCGCAGAGCCAGTGAGCATGACCCCCAGACAGTGAATGCTACTACCTTCCAACTAAGAATGAGATC
GTCTCTCCCCCTGGCATCTCGCAGGCCCTTCTATGCCCGCAACCCCAAGGCCCTGAACCTCGGTGGCATC
GGTGTGCTCATGGCCCATGAGTTGACCATGCTTGTATGACCAAGGGCGGAGTATGAGAAGAGGGAACTCTG
CGGCCCTGGTGCAAGTGAAGTCCCTGGCAGCTTCCGGAACCAAGGGCTCTATGAGGAAACAGTACAATCAA
TACCAGGTCAATGCTTACAAGCATGCTGAGAAAGCATGGGAGGAGCAGCACTGCGAGCCGTGGGGCTCAAG
AACCCAGCTCTTCTTGGTGGGATTTGCCAGGTGTGCTGCTCGGTCGACACAGAGAGCTCTCAGAGGGG
CTGGTGAACGACCCCAAGCCCTGCCCGCTTCCCGTGTGCGGCACTCTCTCAACTCCGCTGACTCTCTGGGG
CACTTCGGCTGCCCTGTGCGCTCCCCATGAACCAAGGCGAGCTGTGTAGGTGTGGTGAACCTGGATCAGGGGA
GAAATGGCCAGCTGTCAACAGACTTGGGCGAGCTCTCTGACAAGAGCTGTTTGTCTCTGGGTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCAAGGTGACATGAGTACAGCCCTCTCAATCACCAATGT
TGCTCTGCTTTGGGGTGCCTGCTCCAGAGAGCCCAACCATTCAGCTGACATCTTTCCGTGTCACCT
GCTGGAAGAGGTCTGGGTGGGAGGCCAGTTTCCATAGGAAGAGTCTGCG

FIGURE 225

MNVALQELGAGSNVGFQKQTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH
STCLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGWIRRNPLDGRSRWNTFNSLWDQNQA
ILKHLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRLDIEKIGGWNITGPDWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLFLPSRDYYLNRTANEKVLTA
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPELSDSEPVVVYGM DYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLETLTYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFFEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMNLNLYNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAGQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPQGQLCEVW

Type II Transmembrane domain:

amino acids 32-57

[illegible][illegible]

FIGURE 227

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGCGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAG
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCCTTGTCGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCTTACAGAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCGTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTTCGA
GGAACCCCTGCCCAGTGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATCTCTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTC AACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAAGTAAGGAAC
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGTCAGAGCAGGAAGGTGAGCCTATCCTGTCACTAGTGAACAACTGCCCT
CCTTTCTTTCTTTCTTTCTTCTCCCTCCCTCCCTTTCTTCCCTTTTCTTCTTCTTCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTGCG
GAGATATAAGTTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCTGAGGATTGAGGAGAGCTTATGGAGCC
AGCAAAGTCTTCTGAAGAGATTGCATTTGAGCCAGGTCTCTGTAG

FIGURE 228

ATGCCTACTACCTTCCAATAAGAATGAGATCGTCTTCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCGCAACCACCCCAAGGCCCTGAACCTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCTTTTGTATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAAATGAGTCCCTGGCAGCCTTCCGGAACCACACGCGCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAAACGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACACGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCAAACCTCCCGTGACTTCCTGCGGC
ACTTCGGCTGCCCTGTGCGCTCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTTGGGTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCTT
GCCTCCAGCAGAGCCCCACCATTCAGTGTGACATCTTTCGGTGTCACCCTGCCTGGAAGAG
GTCTGGGTGGGAGGCCAGTTCCTATAGGAAGGAGTCTGCCTCTTCTGTCCCAGGCTCACT
CAGCCTGGCGGCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCACACTTAGGGGTGGAAGTCACTCTGTCT
TGGCTCACCCCTCAGGGCTACCCCCACCTCACCCCTGTGCTCCTTGTGCCACTGCTCCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTTGAAAGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGTACTGGTTCTGTG
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

[illegible]

CCACAGCGTCCGAGGCGCCCGGAGAATTAGACACACTCCGGACGCGGGCAAAGCAACCGGAGA
GGAGGGGGAGGCAAAAACACCGAAAAACAAAGAGAGAGAAACACCAACCAACCACTTGGGGTGG
GGGGAAGAAAGAAAGAAAGAAACCCACCCACCCAAACCAAAAAAAGAAAAA
AAAAAAGAAAAATCCTGTGGCGCGCCGCTGGTTCCGGGGAAGACTCGCCAGCACCAGGGGG
TGGGGGAGTGCAGAGCTGAAGAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGAGTGAGCATATGATGAT
CTGTTGGTGTCAGGGGTGCTGTTGCTCGAAGAGCTGGCTGGCGCGGTGCTCTCAGCCTGTG
CTGCGCTGCTACCTCTCGCTCCCGGCTGGACAGAGTGTTGGAATCTCCCTGGGGCGCTGGG
ACAACATGATGGTCAAGAAAGGGACACGGCGGTGAGTCTAGGTGTTATTGGAAGATGGAGCT
TCAAAGGTGCTGGCTGGAACCGGTCAAGTATTATTTTGGGGAGGTGATAAGTGGTCAG/
GGATCTGCGATTTCATTTCAACATTGAATAAAGGGACTACAGCTCCAGATACAGAATG
TAGATGTGACAGATGATGGCCCATACAGTGTCTGTCTGACATCAACATACCCAGAAGA
ATGCAAGGTGCATCTAACTGTGCAAGTCTCTCTAAGATATATGCATCTCAAATGATATGC
CTTCAATGAAGGAACCAACCGCTACTCTTACTGTTTGGCCACTGCGGAACCCAGAGCGCTTCCA
TGCTTTGGCGACACATCTCCCCTACGAAAAACATTGTGAAATGGACAATATTGTGCACATT
TATGGAATTACAAGGGACAGGCTGGGGAATAGAAATGCAGTGCGGAAAACTGCTGTGTCATT
CCCCAGATGTGAGGAAGTAAAGATTGTTGTCAACTTTGCTCTCTACTATTCCAGAAATTAAT
CTGGCACCGTGACCCCGGACGAGCTGGCCCTGAATAAGATGTAAGGTGCAGGTGTGGCGCT
CCAGCTTTTGAATTGGTACAAAGGAGAGAAGAGCTCTTCAATGGCCCAACGAAGGAATTATAT
TCAAATTTTGTGACAGAAGATCCATTCTCACTGTACCAACGTGACAGGACACTTCCGGCA
ATTATACCTGTGTGGCTGCCAACAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCT
CCAAGTACAGCCAGTATGGAATTACCGGAGAGCGTGATGTTCTTTCTCTGCTGGTCACT
TGTTGTGACATGCTCTCTTTCCACAGCAATTTCTACTGAGAAGTGCATTTCAACAATAA
TTCAAAGACCCATAAAAGGCTTTTAAAGGATTCTGAAAGCTGCTAGGCTGGATCCAATCT
GGTACAGTTTGTAAAAGCAGCGTGGGATATAATCAGCAGTGTCTACATGGGATGATCGCT
TCTGTAGAATTGCTCATATTGTATAAATCTTTAATTCTACTCTTTTGTATAGTACATTA
CCTTGTGAAGCAGTACAGATTGCTCTTTTTTAAAGACGTGAAGAGTGTGAATATTCTTTAG
AGGATATTAAATTGTAAATTTCATGTTTGAATCTCAACAATTTCAAAGCATTCAGTATGCT
CTGCTAGGTTGCGAGCTGTAGTTTACAAAAACGAATATTGTCAGTGAATATGTGATTCTTAA
GGCTGCAATACAGCAATTCAGTTCTCTGTTTCAATAAGAGTCAATCCACATTTACAAGATG
CATTTTTTTCTTTTGAATAAAAGCAATAATTTGCCTTAGATATTCTTTCAAATA
TAACACATATCTAGATTTTCTGCTTGCATGATATCTCAGTTTCAGGAATGAGCCTTGTAT
AATCTGGCTGTGCGAGCTCTGCTCTCTTTCTGTGAAGTTACAGATGGGTGCTCTTCAT
ATAATATTCTTCTCTTTGTCTTCAATATAAAGATTGTTTGTCTAAATCTTCAATTTGA
AAGTAAAAATAAACAGAGTATCAGTTTAAACATACATCTCTAAGTATGACGAAGAGC
TATTGGACTGTAAAAATCTCTTCTGCATGCAATGGGTTTGAGAAATTTGCCCCACAT
AATCAGTTCTTGTGATGAGAGACAATTAAACAGTATGAAATATACCATATGATTTC
TTGCTGTGATGCTAAATGCTGTAGATCACCGTGGAAATCTCCCTTTAAATGACAGCACA
TGCTACTCAAGGATGGCTAGCAATACGACATCTTTTCTTCACTAGTCCAAGCCAAAAA
TTTTAAGATGATTTGTGCAAGAGGGCACAAGACTATCACCTAATATACGAAGGTTGGTA
AGCGCTCATCATTTAATTTTATTTTGTGGCAGGTATTATGACAGTGCAGCTGGAGGGTATGTA
TATGATATGGACGTTCCAGAGACTAATATGGCAGAAACAGGGTGGTTATGACCGCTATCT
AGGAGGAATACAGACAAATATGACCACTGAATGAGACATGCACATATATAGATACA
CAAGGAATAATTTCTGATCCAGATGCTCTTCAACATGGCTGTTATTATAAGGTTTTTGG
AGCTGCCTGAAGCATCTTATTTATAGTATATCAACCTTTTGTTTTAAATTGACCTGCCA
AGGTAGTGAAGACCTTTAGACAGTTCATCTTTTTTTAAATTTTCTGCTCTATTTTAA
AGCAAAATATGGGACGTTTGTCAAAAAAAGAAAAAAGAAAAA

FIGURE 230

MMLLVQGACCSNQWLA AVL LSLCCLLP SCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED
GASKGAWLNRSS IIFAGGDKWSV DPRVSI STLNRDYS LQIQNV DVTDDGPY TC SVQTQHTP
RTMQVHLTVQVPPKIYDISNDMTVNEG TNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYECSAENAVSFDPVRKVKVVNFAPT IQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKL GTTNASLPL
NPPSTAQYGITGSADVL FSCWYLVLTLSSFTSIFYLKNAILQ

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

Myelin P0 protein:

amino acids 92-121

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCCTCTTGAGGGGAGCATTCTCTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAGAATAAGAAAATTCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCCAAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTCGAAA
TCAATGTTCCAAAGCCCAGAGGAGAAAATGGGGTGAACTTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC
GCGGCTCCGGGTCTTGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG
CAAGTCCTGCAGGCCCAACTCACCTGGGTCCGCTCAGCCATGAGCACTTGCTGCAGCGGGT
AGACAACCTTACTCAGAACCAGGGATGTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTC
TTCAAGGTCAAAAGGGGGCCATGGGCATGCCCTGGTGCCCTGGCCCGCCGGGACCACCTGCT
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTTCGGGACCCCAAGG
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCAGGGTGCTCCAGGGAAGCAAG
GAGCCACTGGCACCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT
GGCCCAAAGGGGAACTGGAACCTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGAGGGCCCTCTGGAGCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCACCAGGTTTGCTGGTCTTCTCTGGAGCTAAAGGAGAT
CAAGGACAACCTGGACTGCAGGGTGTTCCGGGCCCTCCTGGTGCACTGGGACACCAGGTGC
CAAGGGTGAGCCTGGCAGTGCTGGCTCCCCTGGCGAGCAGGACTTCAGGGGAGCCCCGGGA
GTCCAGGAGCCACAGGCTGAAAGGAAGCAAAGGGGACACAGGACTTCAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG
GCTGCGAGGTCCAAAGGAGCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGTGAAAGAGGTGAAAACTCAGTGTCC
GTCAGGATTGTGGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG
GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGATGCTGGGTT
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
GTTCAGTGTGGGGCAGCGAGAGTACCCTGTGTGAGCTGCACCAAGAATAGCTGGGGCCATCA
TGACTGCAGCCACGAGGAGGACGAGGCGTGGAGTGCAGCGCTGGAACCGGAAACCCTTTCA
CTTCTGTCTCCGAGGTGTCTCCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAAATAAGCTCAACATCATTGA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAPHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD
GATGPSGPQGGPPGVKGEAGLQGPQGAAPGKQGATGTPGPQGEKGSKDDGLIGPKGETGTKE
KGDGLGLPGSKGDRGMKGDAGVMGPPGAQGSKGDFFRPGPPGLAGFPGAAGDQGGPGLQGVPG
PPGAVGHGPAKGEPPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTGLQGGQGRKGESGVPGPA
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLW
SCTKNSWGHHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACCTACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTCAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACCTGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCCAAAAGACGTTTCTTTGGACCAAAGATCTCTTTG
TGATTCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTT
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1 .

MKLMVLVFTIGLTLLLGVQAMPANRLSCYRKILKDHNCNHLPEGVADLTQIDVNVQDHFWDG

KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTTCTGGAGCGAATTCAGCCTGCAGGG
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCGTGGTGGTTGGAGGGC
 CGCGAGTAGACGACGACACAGCGCGGGTCCCGGGAGGGCGGGTCTGCTCGCGCCGAGATG
 TGGAAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCGCGCTGGCTGTG
 CGCTGGGGCGCTGGTGTGCGGGGTGGCTTCTTTCTCCTCGGCTTCTCTTCGCGGTGGTTA
 TAAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGAT
 GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC
 AGGAACAGAACAAATCTTTCAGCTTGCAAAGCAAATTCAAATCCAGTGGAAAGAAATTTGGCC
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCCTGTTGTCTTACCCAAATAAGACTCATCCC
 AACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTATTTTGAACC
 ACCTCCTCCAGGATATGAAATGTTTCGGATATGTAACACCTTTTCAGTGTCTTCTCTCCTC
 AAGGAATGCCAGAGGGCGATCTAGTGATGTTAACTATGCACGAACTGAAGACTTCTTTAAA
 TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTTGTAATTTGCCAGATATGGGAAAT
 TTTTCAGAGGAAAATAGGTTTAAAAATGCCAGCTGGCAGGGGGCCAAAGGAGTCATTCTCTACT
 CCGACCTGTCTGACTACTTTTGTCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCT
 GGAGGTGGTGTCCAGCGTGGAAAATCTCTAAATCTGAATGGTGCAGGAGACCTCTCACACC
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAAATTCAGAGGCTGTTGGTCTCCAA
 GTATTCTGTTTCATCCAAATGGGATACATGATGCACAGAAGCTCCTAGAAAAATGGGTGGC
 TCAGCACCACAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG
 CTTTACTGGAACCTTTTCTACAAAAAGTCAAGATGCACATCCACTTACCAATGAAGTGA
 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAAACAGACAGATATGTCATT
 CTGGGAGGTACCGGGACTCATGGGTGTTTGGTGGTATTGACCCCTCAGAGTGGAGCAGCTGT
 TGTTTCATGAAATTTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA
 CAATTTGTTTGAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCCTAGTGGGGCA
 GAGGAGAATTCAGACTCTTCAAGAGCTGCGCTGGCTTATATTAATCTGACTCATCTAT
 AGAAGGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAAATCTCTTTATGAAAGTTGG
 ACTAAAAAAGTCTCTCCCGAGGTTTCAGTGGCATGCCAGGATAAGCAAATGGGATCTGG
 AAATGATTTTGAGGTGTTCTTCCAACGACTTGGAAATGCTTCAGGCAGAGCAGGTATACATA
 AAAATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT
 GAGTTGGTGGAAAAGTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCCGAGTTTCG
 AGGAGGGATGGTGTTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGATTGTGAGATATATG
 CTGTAGTTTAAAGAAATATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA
 ATGAAGACATACAGTGTATCATTGATTCACTTTTTTCTGCAGTAAAGAAATTTTACAGAAAT
 TGCTTCCAAGTTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCATAGTATTAAAGAA
 TGATGAATGATCAACTCATGTTTCTGGAAGAGCAATTTATGATCCATTAGGGTTACCAGAC
 AGGCCTTTTATAGGCATGTATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC
 ATTCACAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCCT
 GGGGAGCAAGTGAAGAGACAGATTTATGTTGCAGCCTTCAGGTGCAGGAGCTGCAGAGACT
 TTGAGTGAAGTAGCCTAAGAGGATTTTATGAGAATCCGATATTGAATTTGTGTGGTATGTCA
 CTCAGAAAGAAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTGAAATAAAGT
 TGAATATTATATATAA

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLETDSAVATARRPRWLCAGALVLAGGFLLGFLFGWFIKSSNEATNITPKHNMKAFL
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH
PNYISIIINEDGNEIFNTSLFEP PPPGYENVSDIVPPPSAFSPQGMPEGDLVYVNYARTEDFF
KLERDMKINCSGKIVIARYGKVFGRGNKVNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQRGNILNLNGAGDPLTPGYPAN EYAYRRGIAEAVGLPSIPVHP IGYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVGP GFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRIY
ILGGHRDSWVFGGIDPQSGAAVVEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW
ABENSRLQERG VAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKE LKSPDEGFEGKSLYES
WTKKSPSP EFGMPRI SKLGS GNDFEVFFQRLGIASGRARYTKN WETNKFSGYPLYHSVYET
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ
EMKTYSVSFDLSLFAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP
DRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713